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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 11:45:41 : Search time 2813 Seconds

(without alignments)
6758.073 Million cell updates/sec

Title: US-10-724-225-1_COPY_1_402

Perfect score: 402
Sequence: 1 ATGTGCAATACCAACATGTC.....ACCTTGAAGTGGAGTGAT 402

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pt: *
10: gb_ro: *
11: gb_sbs: *
12: gb_sy: *
13: gb_un: *
14: gb_vt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	646	9 AF385323	AF385323 Homo sapi
2	402	100.0	652	6 AR207094	AR207094 Sequence
3	402	100.0	659	9 HSA491698	AJ491698 Homo sapi
4	402	100.0	729	6 A61763	A61763 Sequence 3
5	402	100.0	729	6 AR264886	AR264886 Sequence
6	402	100.0	732	9 HSA430612	AJ430612 Homo sapi
7	402	100.0	852	6 A44504	A44504 Sequence 4
8	402	100.0	1476	6 A61359	A61359 Sequence 1
9	402	100.0	1476	6 AX057138	AX057138 Sequence
10	402	100.0	1476	6 AX695559	AX695559 Sequence
11	402	100.0	1476	9 BT007258	BT007258 Homo sapi
12	402	100.0	1476	12 BT007935	BT007935 Synthetic
13	402	100.0	2372	6 CO717844	CO717844 Sequence
14	402	100.0	2372	6 AR000256	AR000256 Sequence
15	402	100.0	2372	6 AR009781	AR009781 Sequence
16	402	100.0	2372	6 AR028963	AR028963 Sequence
17	402	100.0	2372	6 AR154584	AR154584 Sequence
18	402	100.0	2372	6 BD233925	BD233925 Method an
19	402	100.0	2372	6 I11727	I11727 Sequence 1

20	402	100.0	2372	6 I12226	I12226 Sequence 1
21	402	100.0	2372	6 I21256	I21256 Sequence 1
22	402	100.0	2372	6 I25341	I25341 Sequence 2
23	402	100.0	2372	6 I36472	I36472 Sequence 2
24	402	100.0	2372	6 I40222	I40222 Sequence 2
25	402	100.0	2372	6 I79856	I79856 Sequence 2
26	402	100.0	2372	6 I86850	I86850 Sequence 2
27	402	100.0	2372	6 AR212312	AR212312 Sequence
28	402	100.0	2372	6 AR214399	AR214399 Sequence
29	402	100.0	2372	6 AX329941	AX329941 Sequence
30	402	100.0	2372	6 AX587651	AX587651 Sequence
31	402	100.0	2372	6 AX695558	AX695558 Sequence
32	402	100.0	2372	6 BD073962	BD073962 Antisense
33	402	100.0	2372	6 BD138075	BD138075 Antisense
34	402	100.0	2372	9 HSP53AS6G	Z12020 H. sapiens m
35	402	100.0	2372	9 HUMS552A	M92424 Human p53-a
36	402	100.0	3121	9 BC067077	BC067077 Homo sapi
37	360.4	89.7	1460	4 AF100705	AF100705 Canis fam
38	358.8	89.3	1469	4 AB031276	AB031276 Canis fam
39	358.8	88.9	1477	4 AF322416	AF322416 Canis fam
40	357.2	88.9	2042	4 AB099709	AB099709 Felis cat
41	355.6	88.5	1476	4 AF121140	AF121140 Equus cab
42	342	85.1	1361	9 AF092844	AF092844 Homo sapi
43	327.4	81.4	388	9 AF092843	AF092843 Homo sapi
44	289.2	71.9	1470	6 AX695556	AX695556 Sequence
45	289.2	71.9	1470	10 MMU47934	U47934 Mus musculi

ALIGNMENTS

RESULT 1

AF385323

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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REFERENCE

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

ORIGIN

Query Match 100.0%; Score 402; DB 9; Length 646;
Best Local Similarity 100.0%; Pred. No. 2.4e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAAACCACTCAGATTCCA 60
DB 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAAACCACTCAGATTCCA 60

QY 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120
DB 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120

QY 121 GTTGTGACAAAAGACACTTATATCTATGAGAGAGTCTTTTATCTTGGCAGTAT 180
DB 121 GTTGTGACAAAAGACACTTATATCTATGAGAGAGTCTTTTATCTTGGCAGTAT 180

QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTCAATGAT 240
DB 181 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTCAATGAT 240

QY 241 CTCTAGAGATTGTTGGTGGCCAGCTTCTCTGTGAAGGACAGAGAAATATAT 300
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QY 301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGAAATCATCGACTCAGTACA 360
DB 301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGAAATCATCGACTCAGTACA 360

QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTAT 402
DB 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTAT 402

RESULT 2
LOCUS AR207094
DEFINITION Sequence 3 from patent US 6372490.
ACCESSION AR207094
VERSION AR207094.1 GI:21505896
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 652)
AUTHORS Nandabalan, K., Yang, M. and Schulz, V.
TITILE Nucleic acid encoding the MDW interacting protein
JOURNAL Patent: US 6372490-A 3 16-APR-2002;
FEATURES
source 1. .652
location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.4e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAAACCACTCAGATTCCA 60
DB 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAAACCACTCAGATTCCA 60

QY 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120
DB 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120

QY 121 GTTGTGACAAAAGACACTTATATCTATGAGAGAGTCTTTTATCTTGGCAGTAT 180
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QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACAATATTGTCAATGAT 240
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QY 301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGAAATCATCGACTCAGTACA 360
DB 301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGAAATCATCGACTCAGTACA 360

QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTAT 402
DB 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTAT 402

RESULT 3
LOCUS HSA491698
DEFINITION Homo sapiens mRNA for p53-binding protein alternatively spliced isoform HB67 (MDM2 gene).
ACCESSION AJ491698
VERSION AJ491698.1 GI:21628666
KEYWORDS alternative splicing; MDM2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bartel, F., Pinkert, D., Kappler, M., Bache, M., Schmidt, H. and Taubert, H.
TITILE Alternatively and aberrantly spliced transcripts of the MDM2 mRNA occur frequently in human soft tissue sarcoma and in multiple normal tissues
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 659)
AUTHORS Bartel, F.
TITILE Direct Submission
JOURNAL Submitted (25-JUN-2002) Bartel F., Institute for Pathology, University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097 Halle, GERMANY
FEATURES
source 1. .659
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="lymphocyte"
1. .659
/gene="MDM2"
1. .501
/gene="MDM2"
/note="alternatively spliced isoform HB67"
/codon_start=1
/product="p53-binding protein"
/protein_id="CAD38959.1"
/db_xref="GI:21628667"
/db_xref="TrEMBL:Q8NDW2"
/translation="MCNTNMSVPTDGAVTTSOIPASEQETLVKPKLILKLSVGAQ KDIYTMKEVLFTYIGYIMTKRILYDEKQIHIVCSNDLGLDGVPSFVKEHRKIYTM IYRNLVYVNOQSSDSGTSVSENKRLBEGSDPKDLVQLQEKPKTKRVMNLVCP L MFLNLV"

ORIGIN
Query Match 100.0%; Score 402; DB 9; Length 659;
Best Local Similarity 100.0%; Pred. No. 2.4e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAAACCACTCAGATTCCA 60
DB 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAAACCACTCAGATTCCA 60

QY 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120
DB 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAGCCATTGCTTTTGAAGTATTAAATCT 120

QY 121 GTTGTGCACAAAAGACACTTATATAGTAAAGAGCTCTTTTATCTTGGCCAGTAT 180
DB 121 GTTGTGCACAAAAGACACTTATATAGTAAAGAGCTCTTTTATCTTGGCCAGTAT 180
QY 181 ATTATGACTAAACGATTATATATAGTAAAGACAAACATATTTGTAATTTGTTCAATGAT 240
DB 181 ATTATGACTAAACGATTATATATAGTAAAGACAAACATATTTGTAATTTGTTCAATGAT 240
QY 241 CTCTTAGAGATTTGTTGGCGGCCAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
DB 241 CTCTTAGAGATTTGTTGGCGGCCAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGCAGAAATCATCGACTCAGTACA 360
DB 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGCAGAAATCATCGACTCAGTACA 360
QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTGTAT 402
DB 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTGTAT 402

RESULT 4
LOCUS A61763 729 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 3 from Patent WO9711367.
ACCESSION A61763
VERSION A61763.1 GI:3715951
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1
AUTHORS Chene, P. and Hochkeppel, H.
TITLE ASSAY FOR IDENTIFYING INHIBITORS OF THE INTERACTION BETWEEN
JOURNAL PROTEINS P53 AND dm2
CIBIA GEIGY AG (CH)
Patent: WO 9711367-A 3 27-MAR-1997;
FEATURES
source location/Qualifiers
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/db_xref="taxon:32644"
84..650
/codon_start=1
/product="N-TERMINAL 188 AMINO ACIDS OF HUMAN DOUBLE
MINUTE PROTEIN 2"
/protein_id="CAA03593.1"
/db_xref="GI:3715952"
/translation="MCNTNMSVPTDGAVTTSQIPASEOFTLVPRKPLLKILKSVGNO
KDTYTKKLVFYLGGYIMTKRLVDKQOHVYCGNDLGLFGVPSVSVEHRIYTM
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ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 60
DB 84 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 143
QY 61 GCTTGGACAAAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAAGTTATTAAGTCT 120
DB 144 GCTTGGACAAAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAAGTTATTAAGTCT 203
QY 121 GTTGTGACAAAAGACACTTATATATGTAAGAAAGAGTCTTTTATCTTGGCCAGTAT 180
DB 204 GTTGTGACAAAAGACACTTATATATGTAAGAAAGAGTCTTTTATCTTGGCCAGTAT 263
QY 181 ATTATGACTAAACGATTATATATAGTAAAGACAAACATATTTGTAATTTGTTCAATGAT 240
DB 264 ATTATGACTAAACGATTATATATAGTAAAGACAAACATATTTGTAATTTGTTCAATGAT 323

QY 241 CTCTAGAGATTTGTTGGCGGCCAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
DB 324 CTCTAGAGATTTGTTGGCGGCCAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 383
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGCAGAAATCATCGACTCAGTACA 360
DB 384 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGCAGAAATCATCGACTCAGTACA 443
QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTGTAT 402
DB 444 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTGTAT 485

RESULT 5
LOCUS AR264886 729 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6492116.
ACCESSION AR264886
VERSION AR264886.1 GI:29693255
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 729)
AUTHORS Chene, P. and Hochkeppel, H.-K.
TITLE Assay for identifying inhibitors of the interaction between
JOURNAL proteins p53 and dm2
Patent: US 6492116-A 3 10-DEC-2002;
FEATURES
source location/Qualifiers
1..729
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 60
DB 84 ATGTGCAATACCAACATGTCTGTACTACTGATGCTGTAAACCACTCAGATTCACA 143
QY 61 GCTTGGACAAAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAAGTTATTAAGTCT 120
DB 144 GCTTGGACAAAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAAGTTATTAAGTCT 203
QY 121 GTTGTGACAAAAGACACTTATATATGTAAGAAAGAGTCTTTTATCTTGGCCAGTAT 180
DB 204 GTTGTGACAAAAGACACTTATATATGTAAGAAAGAGTCTTTTATCTTGGCCAGTAT 263
QY 181 ATTATGACTAAACGATTATATATGTAAGAAAGAGTCTTTTATCTTGGCCAGTAT 240
DB 264 ATTATGACTAAACGATTATATATGTAAGAAAGAGTCTTTTATCTTGGCCAGTAT 323
QY 241 CTCTAGAGATTTGTTGGCGGCCAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
DB 324 CTCTAGAGATTTGTTGGCGGCCAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 383
QY 301 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGCAGAAATCATCGACTCAGTACA 360
DB 384 ACCATGATCTACAGAACTTGTAGTAGTCAATCAGCAGAAATCATCGACTCAGTACA 443
QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTGTAT 402
DB 444 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGTGTAT 485

RESULT 6
LOCUS HSA430612 732 bp mRNA linear PRI 15-FEB-2002
DEFINITION Homo sapiens mRNA for MDM2 isoform KB9.
ACCESSION AJ430612

VERSION	KEYWORDS
AJ30642.1	GI:18698329
Lymphocytes; MDM2 isoform KB9.	
SOURCE	ORGANISM
Homo sapiens (human)	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	AUTHORS
1	Bartel,F., Pinkert,D., Kapler,M., Bache,M., Schmidt,H. and Tadebl,H.
Tadbl,H.	Alternatively and Aberrantly Spliced Transcripts of the MDM2-mRNA Occur Frequently in Human Soft Tissue Sarcomas and in Multiple Normal Tissues
JOURNAL	REFERENCE
Unpublished	2 (bases 1 to 732)
Bartel,F.	Direct Submission
Submitted (12-FEB-2002)	Bartel F., Institute for Pathology, University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097 Halle, GERMANY
FEATURES	source
location/Qualifiers	
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/tissue_type="lymphocytes"	
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/gene="MDM2 isoform KB9"	
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/translation="WCNTNMSVPTDGAVTTSQIPASEGETLVREKPLLKLKLSVGAGKDYTNSATLKVLFYLGQIYMTKRLLYDEKQOHIVYGNDLIGDFGVPSVSKHRKIYTMIRYLVVNQSSDSGTSVENRCHLEGSDODVLQELBEKRSSSHIVSRPSTSSRRRIISFEETQDDKBESVESLLPLNAIEPCVVICGRPNNGCIYHGKHLMACFTCAK KLKRNKCPICRPDIQIVLTYP"	
ORIGIN	Query Match
	100.0%; Score 402; DB 9; Length 732;
	Best Local Similarity 100.0%; Pred. No. 2.3e-93;
	Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 ATGTGCATTACCACATCTGTCTACTAATGCTGTGTAACCACTCACAGATTCCA 60
Dd	1 ATGTGCATTACCACATCTGTCTACTAATGCTGTGTAACCACTCACAGATTCCA 60
Oy	61 GTTCGGAAACAAGAACCCCTGTTGACCAAAAGCATTCCTTTTGAAATTATAAGTCT 120
Dd	61 GTTCGGAAACAAGAACCCCTGTTGACCAAAAGCATTCCTTTTGAAATTATAAGTCT 120
Oy	121 GTTGTGCACAAAAGAAGACACTTATATCTATGAAGAAGTCTTTTTTATCTTGGCAGAT 180
Dd	121 GTTGTGCACAAAAGAAGACACTTATATCTATGAAGAAGTCTTTTTTATCTTGGCAGAT 180
Oy	181 ATTATGATTAACGATTATATGATGAGAAGCAACAATATGATATTTGTTCAAATGAT 240
Dd	181 ATTATGATTAACGATTATATGATGAGAAGCAACAATATGATATTTGTTCAAATGAT 240
Oy	241 CTTTAGAGAGATTGTTGGCGTGCCAAGCTTCTCTGTGAAGAAGCAAGAAAAATATAT 300
Dd	241 CTTTAGAGAGATTGTTGGCGTGCCAAGCTTCTCTGTGAAGAAGCAAGAAAAATATAT 300
Oy	301 ACCATGATCTACAGAACTTGATAGTCAATACAGAGATCATCGACTCAGGTACA 360
Dd	301 ACCATGATCTACAGAACTTGATAGTCAATACAGAGATCATCGACTCAGGTACA 360
Oy	361 TTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGATGAT 402
Dd	361 TTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGATGAT 402

[illegible]

COMMENT RHONE POULENC RORER SA (FR)
Other publication FR 2738151 970307.
FEATURES location/Qualifiers
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KDTYMEKVLFLGQYIMTRKLYDEKQOHLYVCSNDLLGLDFGVPSFVSKRITVM
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RRARISTEENSDELSEGRORRKHKSISLSFDESLALCVIREICCRSSSESTGT
PSNPDLDAGVSEHSGDWLDDSDVSDFSEVEVSLSESDYLSLEGGESLDEDEYV
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ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACCACTCAGATTCCA 60
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Db 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACCACTCAGATTCCA 60
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Oy 61 GCTTGGACAAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
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Oy 121 GTTGGTCACAAAAGACCTTATATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
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Oy 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGTGGAGTGTAT 402
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Db 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGTGGAGTGTAT 402
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RESULT 9
AX057138 1476 bp DNA linear PAT 17-JAN-2001
LOCUS AX057138
DEFINITION Sequence 14 from Patent WO0075184.
ACCESSION AX057138
VERSION AX057138.1 GI:12309959
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Zhang, H., Tsvetkov, L.M., and Kondo, T.
TITLE Modulation of protein levels using the scf complex
JOURNAL Patent: WO 0075184-A 14 14-DEC-2000;
VALE UNIVERSITY (US)
FEATURES location/Qualifiers

source

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/note="unnamed protein product; Human MDM2"
/codon_start=1
/protein_id="CAC22426.1"
/db_xref="GI:12309960"

CDS

1..1476
/translation="MCHTMSVPPDGAVTTTSQIPASRQETLVPRKPLLKLLKSVGAQ
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IYRNLVYVNOEESDSCGTSVENRCHLEGGSDQDLVQELQOEKPSSSHVSRSTSS
RRARISTEENSDELSEGRORRKHKSISLSFDESLALCVIREICCRSSSESTGT
PSNPDLDAGVSEHSGDWLDDSDVSDFSEVEVSLSESDYLSLEGGESLDEDEYV
QVTVYQAGEBDTDSFEEDPEISLADYVKCTSCNMNPLPSHCNRCHALRENNMLPEBK
GKDGEISEKAKLENSTQAEFGFVDPCKKITVNDRESCEVEENDKITQASQOSE
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ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACCACTCAGATTCCA 60
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Db 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTAAACCACTCAGATTCCA 60
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Oy 61 GCTTGGACAAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
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Db 61 GCTTGGACAAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
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Oy 121 GTTGGTCACAAAAGACCTTATATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
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Oy 241 CTTCTAGAGATTGTTGGCGTGCACAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
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Oy 301 ACCATGATCTACAGAACTTGTAGTATGATCAGACGAATATCGACTCAGTACA 360
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Db 301 ACCATGATCTACAGAACTTGTAGTATGATCAGACGAATATCGACTCAGTACA 360
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Oy 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGTGGAGTGTAT 402
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Db 361 TCTGTGAGTGAGAACAGGTGTACCTTGAAGTGGAGTGTAT 402
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|
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RESULT 10
AX695559 1476 bp DNA linear PAT 31-MAR-2003
LOCUS AX695559
DEFINITION Sequence 1186 from Patent WO03008583.
ACCESSION AX695559
VERSION AX695559.1 GI:29418711
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Morris, D.W. and Engelhard, E.K.
TITLE Novel compositions and methods for cancer
JOURNAL Patent: WO 03008583-A 1186 30-JAN-2003;
Segre Discovery (US)
FEATURES location/Qualifiers
source 1..1476
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ORIGIN

/db_xref="taxon:9606"

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Db	61	GCTTCGGAAACA	GAGACCCCTGGTTA	AGACCAAAAGCCAT	GCTTTTGAAGTTA	ATTAAGTCT	120
QY	121	GTTGGTGCACAAA	AAAGACCTTATCTA	TATGAAAAGGTTCT	TTTTTATCTTGGCCAGAT		180
Db	121	GTTGGTGCACAAA	AAAGACCTTATCTA	TATGAAAAGGTTCT	TTTTTATCTTGGCCAGAT		180
QY	181	ATTATGACTAAAC	GCATTTATATGATG	AGAAAGCAACAATAT	TGTATATGTTTCAATGAT		240
Db	181	ATTATGACTAAAC	GCATTTATATGATG	AGAAAGCAACAATAT	TGTATATGTTTCAATGAT		240
QY	241	CTTCTAGAGATTT	GTTTGGCGTGCCA	AGCTTCTCTGTGAA	AGAGCAGAGAAAATATAT		300
Db	241	CTTCTAGAGATTT	GTTTGGCGTGCCA	AGCTTCTCTGTGAA	AGAGCAGAGAAAATATAT		300
QY	301	ACCATGATCTTA	CAGGAATTGGTAGT	CAATCAGCAGAAATC	ATCGGAATCGAGATTC	CAAGTACA	360
Db	301	ACCATGATCTTA	CAGGAATTGGTAGT	CAATCAGCAGAAATC	ATCGGAATCGAGATTC	CAAGTACA	360
QY	361	TCTGTGAGTGA	AGAACAGGTGCAC	CTTGAAGGTGGAGATGAT		402	
Db	361	TCTGTGAGTGA	AGAACAGGTGCAC	CTTGAAGGTGGAGATGAT		402	

RESULT 11	
BT007258	
LOCUS	1476 bp mRNA linear PRI 13-MAY-2003
DEFINITION	Homo sapiens Mdm2, transformed j773 cell double minute 2, p53 binding protein (mouse) mRNA, complete cds.
ACCESSION	U00000

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1476)	Kalnina, N., Chen, X., Rolfs, A., Halleck, A., Hines, J., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labaer, J., Lin, Y., Phelan, M. and Farmer, A.	Cloning of human full-length CDS in BD Creator (TM) System Donor

FEATURES

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1. .1476

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/db_xref="GI:30583355"
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IYRLNLVVNQESSDSGTSVSENKCHLEGGSDQKDLVQELQEKFPSSSHLVSRPSTE

ORIGIN

Query Match	100.0%	Score 402;	DB 9;	Length 1476;
Best Local Similarity	100.0%	Pred. No. 2.3e-93;		
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Db	61	GCTTCGGAACAAGAGACCCCTGGTTAGACCAAAAGCCATTGCTTTGAACTTAATAAGTCT	120
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Db	121	GTTGGTGCACAAAAGACCTTAATACATATGAAAGAGTTCTTTTATATCTGGCCAGAT	180
Qy	181	ATTATGACTAAAGCATTATATGATGAGAGAACAAACATATTTGATATTTGTTCAATGAT	240
Db	181	ATTATGACTAAAGCATTATATGATGAGAGAACAAACATATTTGATATTTGTTCAATGAT	240
Qy	241	CTTCTAGAGATTGTTGGCGGTCCAAAGCTTCTCTGTGAAGAAGCAGCAAGAAATATAT	300
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Qy	301	ACCATGATCTACAGGAACCTGGTAGTATCATACAGCAGAAATCATCGGACTCAGGTAC	360
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Qy	361	TCGTGAGTAGAACAAGGTGCACTTGAAGAGTGGAGTGAAT	402
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RESULT	12
BT007935	
LOCUS	
DEFINITION	BT007935 1476 bp mRNA linear SYN 13-MAY-2001
ACCESSION	Synthetic construct Homo sapiens Mdm2, transformed 3f3 cell double
VERSION	Euro7935 minute 2, p53 binding protein (mouse) mRNA, partial cds.
KEYWORDS	BT007935.1 GI:30584708
SOURCE	FLI CDNA.
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1 (bases 1 to 1476)
	Kainline,N., Chen,X., Rolfs,A., Hallack,A., Hines,L., Eisenstein,S.,
	Koundiny,M., Raphael,J., Moreira,D., Kelley,T., Labber,J., Lin,Y.,

```

TITLE
Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator (TM) System Donor
vector

JOURNAL
Unpublished
2 (bases 1 to 1476)
Kainine,N., Chen,X., Rolfe,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,D., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,
Phelan,M. and Farmer,A.

REFERENCE
Direct Submission
Submitted (13-May-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

COMMENT
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion in C-terminal
tag). The CDS has been directionally cloned using BD in-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL1
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/offclonea.

FEATURES
Location/Qualifiers
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		IYNRVLVVNQOESSDSGSVENRKLEGGSDODLOVELEKRPSSSHILSRPSTSS
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		GKDGEISEKKALKENSTDAEEGFVPDPCKKITVDNRSCVCEENDDKITQASQOSESD
		DYSPSTSSSIIVYSODEVKEFEREEETQDKSESVELSPLAIIPCVIQCPRPNGCIT
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OY	61 GCTTCGGAACAAGAAGACCCCTGGTTAGAACCAAGGCATTGCTTTGAAGATTATTAAGTCT	120
DB	61 GCTTCGGAACAAGAAGACCCCTGTTTAGACCAAGGCATTGCTTTGAAGATTATTAAGTCT	120
OY	121 GTTGGTGCACAAAAGAACACTTATATCTATGAAAGAGGTTCTTTTTTATCTTGGCCAGTAT	180
DB	121 GTTGGTGCACAAAAGAACACTTATATCTATGAAAGAGGTTCTTTTTTATCTTGGCCAGTAT	180
OY	181 ATTATGACTAAAGCATTTATATGATGAGAGCAACAATATTGTTATTTGTTCAAATGAT	240
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OY	241 CTTCTAGAGATTTGTTGGGTGCCAAGCTTCTCTGTGAAAGGCAACGAAAAATATAT	300
DB	241 CTTCTAGAGATTTGTTGGGTGCCAAGCTTCTCTGTGAAAGGCAACGAAAAATATAT	300

OY	301	ACCATGATCTCA	CAGGAAC	CTTGSTAGT	AGTACAA	TACAGACGA	AAATCATCGGAT	CAGGTACA	360
Db	301	ACCATGATCTCA	CAGGAAC	CTTGSTAGT	AGTACAA	TACAGACGA	AAATCATCGGAT	CAGGTACA	360
OY	361	TCCTGTGAGTGA	GGAACAGG	GTGCACCTTGA	AGAGTGAGT	AT	402		
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RESULT 13									
LOCUS	CQ717844								
DEFINITION	Sequence 3778 from Patent WO02068579.								
ACCESSION	CQ717844								
VERSION	CQ717844.1								
KEYWORDS	GI:42278701								
SOURCE									
ORGANISM	Homo sapiens (human)								
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
REFERENCE	1								
AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.								
TITLE	Kits, such as nucleic acid arrays, comprising a majority of								
	humanexons or transcripts, for detecting expression and other uses								
	thereof								
JOURNAL	Patent: WO 02068579-A 3778 06-SEP-2002;								
	PE Corporation (NY) (US)								
FEATURES	location/Qualifiers								
Source	1..2366								

[illegible]

VERSION AR000256.1 GI:3962787
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burdell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Method of diagnosing Neoplastic disease by detecting increased expression of human MDM2 protein
JOURNAL Patent: US 576338-A 2 07-Apr-1998;
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2,2e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCTTCGGAACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAATTAAAGTCT 120
DB 372 GCTTCGGAACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAATTAAAGTCT 431
QY 121 GTTGTGACAAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGACAAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGATATTTGTTCAATGAT 240
DB 492 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGATATTTGTTCAATGAT 551
QY 241 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGAGCAGAGAAATATAT 300
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QY 301 ACCATGATCTACAGAACTTGTAGTCAATCAGCAGAAATCATCGACTCAGGTACA 360
DB 612 ACCATGATCTACAGAACTTGTAGTCAATCAGCAGAAATCATCGACTCAGGTACA 671
QY 361 TCTGTAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
DB 672 TCTGTAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 713

RESULT 15

AR009781 AR009781 2372 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 2 from patent US 5756455.
ACCESSION AR009781
VERSION AR009781.1 GI:3968586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Kinzler, K.W. and Vogelstein, B.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5756455-A 2 26-May-1998;
FEATURES Location/Qualifiers
Source 1..2372
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ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 2,2e-93;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTACTGATGTGCTGTAAACAACCTTCACGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACTACTGATGTGCTGTAAACAACCTTCACGATTCCA 371
QY 61 GCTTCGGAACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAATTAAAGTCT 120
DB 372 GCTTCGGAACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAATTAAAGTCT 431
QY 121 GTTGTGACAAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGACAAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTTGATATTTGTTCAATGAT 240
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QY 241 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGAGCAGAGAAATATAT 300
DB 552 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGAGCAGAGAAATATAT 611
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DB 612 ACCATGATCTACAGAACTTGTAGTCAATCAGCAGAAATCATCGACTCAGGTACA 671
QY 361 TCTGTAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
DB 672 TCTGTAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 713

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Job time : 2820 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 11:45:41 ; Search time 982 Seconds
(without alignments)
2148.948 Million cell updates/sec

Title: US-10-724-225-1_COPY_1_402

Perfect score: 402

Sequence: 1 ATGTGCAATACCAACATGTC.....ACCTTGAAGTGGAGTGAT 402

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: geneseqn2002bs:.*
8: geneseqn2003as:.*
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10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	100.0	652	3	AAa75042 CDNA enco
2	402	100.0	852	3	AAQ92515 Human dou
3	402	100.0	852	2	AAQ87261 Murine dou
4	402	100.0	1476	2	AAE61637 Human MDM
5	402	100.0	1476	4	AAc84596 Human MDM
6	402	100.0	1476	9	ADa02668 Human MDM
7	402	100.0	1476	10	ADb72406 Human MDM
8	402	100.0	1476	10	ADe95916 Human MDM
9	402	100.0	2371	12	ADN71935 MDM2 enco
10	402	100.0	2372	2	AAQ49891 Human MDM
11	402	100.0	2372	2	AAQ94589 Human MDM
12	402	100.0	2372	2	AAE45151 Human MDM
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16	402	100.0	2372	2	AAV28876 Human MDM
17	402	100.0	2372	2	AAV04836 CDNA sequ
18	402	100.0	2372	2	AAV03607 CDNA sequ
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20	402	100.0	2372	2	AAZ37471 Human sar
21	402	100.0	2372	2	AAx35093 Nucleicid

ALIGNMENTS

22	402	100.0	2372	3	AAa29389
23	402	100.0	2372	4	AAE80625
24	402	100.0	2372	4	AAQ07530
25	402	100.0	2372	5	AAE29240
26	402	100.0	2372	6	ABL62113
27	402	100.0	2372	6	AAE42713
28	402	100.0	2372	6	ABV94130
29	402	100.0	2372	6	AAE43913
30	402	100.0	2372	9	ADa02667
31	402	100.0	2372	10	ADb72405
32	402	100.0	2372	10	ADb21436
33	402	100.0	2372	10	ADb95915
34	402	100.0	2372	10	ADb64976
35	402	100.0	2372	12	ADL23892
36	402	100.0	2372	12	ADb52352
37	402	100.0	2372	12	ADP10606
38	402	100.0	2372	12	ADQ19416
39	402	100.0	3190	4	AAK51460
40	402	100.0	3889	12	ADQ23643
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42	299	74.4	2174	10	ADJ95151
43	289.2	71.9	1470	9	ADa02665
44	289.2	71.9	1470	10	ADb72403
45	289.2	71.9	1470	10	ADb21759

ALIGNMENTS

RESULT 1	AAa75042
ID	AAa75042 standard; CDNA; 652 BP.
AC	AAa75042;
DT	02-JAN-2001 (first entry)
DE	CDNA encoding a human MDMIP-binding MDM2 polypeptide fragment.
XX	Human; MDM2 interacting polypeptide; MDMIP; MDM2; cell cycle progression;
KW	cell differentiation; cancer; sarcoma; glioma; squamous cell carcinoma;
KW	breast cancer; astrocytoma; leukemia; lymphoma; tumorigenesis;
KW	gene therapy; ss.
XX	Homo sapiens.
OS	Homo sapiens.
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FH	Location/Qualifiers
FT	1..652
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XX	23-FEB-1999; 99US-0121192P.
PR	03-MAR-1999; 99US-0122643P.
PR	22-FEB-2000; 2000US-00510252.
XX	
XX	(CURA-) CURAGEN CORP.
PA	
XX	
XX	Nandabalan K, Yang M, Schulz VP;
PI	
XX	
XX	WPI; 2000-558398/51.
DR	P-PSDB; AAB08846.
XX	
XX	Novel MDM2 interacting protein useful for treating or preventing
PT	diseases involving aberrant levels of MDM2 and/or MDM-interacting
PT	proteins, comprises a specific amino acid sequence.
XX	

PS Disclosure; Fig 2A; 78pp; English.

XX The present sequence encodes a fragment of a human MD2 polypeptide, which binds to a human MD2 interacting polypeptide (MDM1P). The protein fragment was used as bait in a yeast two hybrid system to identify MDM1P. CC The MDM1P polypeptide is useful for detecting and removing MD2 CC polypeptides in a biological sample by forming MD2-MDM1P complexes. CC MDM1P and MD2 are useful to identify compounds or other agents which CC modulate the activity of MD2 and/or MDM1P-mediated processes. Agents CC that modulate the function of MDM1P/MD2 complexes are useful for CC treating and preventing a disease or disorder involving aberrant levels CC of MD2 or MDM1P. MDM1P is also useful for treating diseases caused by CC aberrant levels of expression of MD2 genes, such as disorders of cell CC cycle progression, cell differentiation, and transcriptional control, CC including cancers such as human sarcoma, glioma, squamous cell carcinoma, CC breast cancer, astrocytoma, leukemia and lymphoma, and tumorigenesis. CC MDM1P and MD2 nucleic acids are useful in gene therapy

XX Sequence 652 BP; 212 A; 116 C; 145 G; 179 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 402; DB 3; Length 652;

Best Local Similarity 100.0%; Pred. No. 1.9e-106; Mismatches 0; Gaps 0;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTAAACCTCAGATTCACA 60

Db 1 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTAAACCTCAGATTCACA 60

QY 61 GCTTCGGAACAGAGACCCCTGGTTAGCCAAAGCCATTGCTTTGAAGTTATTAAGTCT 120

Db 61 GCTTCGGAACAGAGACCCCTGGTTAGCCAAAGCCATTGCTTTGAAGTTATTAAGTCT 120

QY 121 GTTGTGTCACAAAAGACCTTATATCATGATGATGATGATGATGATGATGATGATGAT 180

Db 121 GTTGTGTCACAAAAGACCTTATATCATGATGATGATGATGATGATGATGATGATGAT 180

QY 181 ATTATGACTAAAGCATTATATGATGAGAGCAACACATATTTGATATTTGTTCAATGAT 240

Db 181 ATTATGACTAAAGCATTATATGATGAGAGCAACACATATTTGATATTTGTTCAATGAT 240

QY 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGGCAACAGAAATATAT 300

Db 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGGCAACAGAAATATAT 300

QY 301 ACCATGATCTACAGAACTTGTAGTATGATGATGATGATGATGATGATGATGATGAT 360

Db 301 ACCATGATCTACAGAACTTGTAGTATGATGATGATGATGATGATGATGATGATGAT 360

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

FT region of the ORF only"

XX DE4339533-A1.

XX 14-JUN-1995.

XX 19-NOV-1993; 93DE-04339533.

XX 19-NOV-1993; 93DE-04339533.

XX (DBK-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Zentgraf H, Klein R, Frey M, Martens R;

XX WPI; 1995-216248/29.

XX P-PSDB; AAR75494.

XX Detection of human double minute gene 2 (hdm-2) antibodies - by

XX the detection of specific cancers.

XX Claim 13; Fig 2; 12pp; German.

XX DNA fragments coding for amino acids 1-284, 58-284 and 58-491 of the hdm-

XX 2 (human double minute 2) gene product are claimed. The overlapping

XX protein fragments contain binding regions for hdm-2-specific antibodies

XX and are useful for identifying such antibodies using a claimed

XX immunosay method. The presence of anti-hdm-2 antibodies is diagnostic

XX of certain forms of cancer, e.g. rhabdomyosarcoma

XX Sequence 852 BP; 271 A; 145 C; 199 G; 237 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 402; DB 2; Length 852;

Best Local Similarity 100.0%; Pred. No. 2e-106;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTAAACCTCAGATTCACA 60

Db 1 ATGTGCAATACCAACATGTCTGTACCTAAGTGTGCTGTAAACCTCAGATTCACA 60

QY 61 GCTTCGGAACAGAGACCCCTGGTTAGCCAAAGCCATTGCTTTGAAGTTATTAAGTCT 120

Db 61 GCTTCGGAACAGAGACCCCTGGTTAGCCAAAGCCATTGCTTTGAAGTTATTAAGTCT 120

QY 121 GTTGTGTCACAAAAGACCTTATATCATGATGATGATGATGATGATGATGATGATGAT 180

Db 121 GTTGTGTCACAAAAGACCTTATATCATGATGATGATGATGATGATGATGATGATGAT 180

QY 181 ATTATGACTAAAGCATTATATGATGAGAGCAACACATATTTGATATTTGTTCAATGAT 240

Db 181 ATTATGACTAAAGCATTATATGATGAGAGCAACACATATTTGATATTTGTTCAATGAT 240

QY 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGGCAACAGAAATATAT 300

Db 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGTGAAAGGCAACAGAAATATAT 300

QY 301 ACCATGATCTACAGAACTTGTAGTATGATGATGATGATGATGATGATGATGATGAT 360

Db 301 ACCATGATCTACAGAACTTGTAGTATGATGATGATGATGATGATGATGATGATGAT 360

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

Db 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

QY 361 TCTGTGAGTGAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

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XX DE Human double minute gene 2 (hdm-2) fragment 1.
XX KW Human double minute gene 2; hdm-2; antibody binding region; antigen;
XX KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; ss.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT 1..852
XX FT CDS /*tag= a
FT /label= Fragment 1
FT /note= "encodes amino acids 1-284 of hdm-2, i.e. the 5'-
FT region of the ORF only"
XX DE DE345249-A1.
XX PN 24-MAY-1995.
XX PD 19-NOV-1993; 93DE-04345249.
XX PF 19-NOV-1993; 93DE-04345249.
XX PR 19-NOV-1993; 93DE-04345249.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PI Zentgraf H, Klein R, Frey M, Martens R;
XX DR WPI; 1995-195167/26.
XX DR P-PSDB; AAR75397.
XX PT New hdm-2 fragments contg. antibody binding region - used to detect
XX PT specific antibodies for diagnosis of cancers, also new DNA sequences
XX PT encoding them.
XX PS Claim 4; Fig 2; 11pp; German.
XX CC DNA fragments coding for amino acids 1-284, 58-284 and 58-491 of the hdm-
XX CC 2 (human double minute 2) gene product are claimed. The overlapping
XX CC protein fragments contain binding regions for hdm-2-specific antibodies
XX CC and are useful for identifying such antibodies. The presence of anti-hdm-
XX CC 2 antibodies is diagnostic of certain forms of cancer, e.g.
XX CC rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)
XX SO Sequence 852 BP; 271 A; 145 C; 199 G; 237 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAATGTCTGTACCTAATGATGCTGTAAACCACTCAAGATTCGA 60
DB 1 ATGTGCAATACCAATGTCTGTACCTAATGATGCTGTAAACCACTCAAGATTCGA 60
QY 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAAAGCATTCCTTTGAAGTTATTAAGTCT 120
DB 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAAAGCATTCCTTTGAAGTTATTAAGTCT 120
QY 121 GTTGTGCACAAAAGACACTTATATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
DB 121 GTTGTGCACAAAAGACACTTATATCTATGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
QY 181 ATTATGACTAAACATATATATGATGAGAGCAACAACTATTTGTTCAAAAGAT 240
DB 181 ATTATGACTAAACATATATATGATGAGAGCAACAACTATTTGTTCAAAAGAT 240
QY 241 CTTTATAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
DB 241 CTTTATAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGAGCAGAGAAATATAT 300
QY 301 ACCATGATCTACAGAAAGCTTGTAGTATGATCAATCAGCAGAAATCATCGAATCACTCAGTACA 360
DB 301 ACCATGATCTACAGAAAGCTTGTAGTATGATCAATCAGCAGAAATCATCGAATCACTCAGTACA 360

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QY 361 TCTGTGAGTGAAGAACAGTGTCACTTGAAGTGGAGTAT 402
DB 361 TCTGTGAGTGAAGAACAGTGTCACTTGAAGTGGAGTAT 402

RESULT 4
ID AAT61637 standard; cDNA; 1476 BP.
XX AAT61637
XX AC AAT61637;
XX DT 16-JAN-1998 (first entry)
XX DE Murine double minute 2 coding sequence.
XX KW Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX KW retinosis; ss.
XX OS Mus musculus.
XX PN M09709343-A2.
XX PD 13-MAR-1997.
XX PF 02-SEP-1996; 96MO-FR001340.
XX PR 04-SEP-1995; 95FR-00010331.
XX PA (RHON ) RHONE POULENC RORER SA.
XX PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX PI Tocque B, Duba-Poterszman M, Wasylyk B;
XX DR WPI; 1997-192837/17.
XX DR P-PSDB; AAM13600.
XX PT Treating cancer with antagonist of oncogenic activity of protein Mdm2 -
XX PT or nucleic acid encoding an antagonist, also viral vectors contg. this
XX PT nucleic acid.
XX PS Claim 2; Page 26-30; 43pp; French.
XX CC This is the nucleotide sequence encoding the mouse Mdm2 (murine double
XX CC minute-2) protein, a 90 kD phosphoprotein which binds and modulates the
XX CC activity of the tumour suppressor protein p53. It has now been shown that
XX CC the mdm2 protein itself has oncogenic properties, especially in a p53-
XX CC null background. Mdm2 is observed to unblock cell cycle arrest in G1
XX CC caused by over-expression of the p107 protein. This is especially done by
XX CC the region covering amino acid 1-134. The invention therefore relates to
XX CC antagonists able to inhibit the oncogenic activity of mdm2. These include
XX CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16
XX CC -25 or 18-23 (AAM13602-6), or fragments of transcription factors e.g.
XX CC pRb, TBP or TAF250, which bind amino acids 1-134 of mdm2. Other
XX CC inhibitors include compounds which disrupt binding to region 135-491 of
XX CC mdm2, e.g. Rb, U5 or the transcription factor E2F. The antagonists are
XX CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,
XX CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other
XX CC hyperproliferative conditions such as retinosis
XX SO Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.5e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAATGTCTGTACCTAATGATGCTGTAAACCACTCAAGATTCGA 60
DB 1 ATGTGCAATACCAATGTCTGTACCTAATGATGCTGTAAACCACTCAAGATTCGA 60
QY 61 GCTTCGGAACAAGAGACCTCGTTAGACCAAAAGCATTCCTTTGAAGTTATTAAGTCT 120

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Db      61  GCTTCGGAACAGAGACCCTGGTTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
Qy      121  GTTGTGACAAAAAAGACACTTATACATATGAAAAGGTTCTTTTATCTTGGCAGTAT 180
Db      121  GTTGTGACAAAAAAGACACTTATACATATGAAAAGGTTCTTTTATCTTGGCAGTAT 180
Qy      181  ATTATGACTAAACGATTATATATGATGAGAACAAACATATTTGTATTTGTTCAATGAT 240
Db      181  ATTATGACTAAACGATTATATATGATGAGAACAAACATATTTGTATTTGTTCAATGAT 240
Qy      241  CTTCTAGAGATTGTTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACACAGAAAAATATAT 300
Db      241  CTTCTAGAGATTGTTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACACAGAAAAATATAT 300
Qy      301  ACCATGATCTACAGGAACCTGTGATGATCAATCAGAGAGATCATCGGACTCGCATGATCA 360
Db      301  ACCATGATCTACAGGAACCTGTGATGATCAATCAGAGAGATCATCGGACTCGCATGATCA 360
Qy      361  TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
Db      361  TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

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RESULT 5
AAC84596
ID AAC84596 standard; DNA; 1476 BP.

XX AAC84596;
XX 02-APR-2001 (first entry)
XX
XX Human MDW2 protein encoding DNA.

XX S-phase kinase associated protein; SKP1, SKP2, SKP2-like protein; ZF;
XX CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
XX Bad; Bcl-2; tumour; cytosolic; ds.

XX Homo sapiens.

XX MO200075184-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000MO-US015449.

XX 04-JUN-1999; 99US-0137494P.

XX (UYVA) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.

XX P-PSDB; AAB48284.

XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,
XX PT involves altering levels of proteins such as S-phase kinase associated
XX PT proteins 1, 2 and cullin/CDC53 proteins.

XX Example; Page 93-95; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
XX CC cell, using proteins selected from S-phase kinase associated proteins 1
XX CC and 2 (SKP1, SKP2), SKP2-like proteins (ZP) and CUL-1 (a member of the
XX CC cullin/CDC5 family of proteins). The method is useful for altering the
XX CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
XX CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
XX CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
XX CC that modulate interactions between SKP and target proteins are useful for
XX CC treating tumours

XX Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 4; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.5e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ATGTGCAATTCACAACTATGTTCTGTAAGTGTGCTGTAAACCACTTCACAGATTCCA 60
Db      1  ATGTGCAATTCACAACTATGTTCTGTAAGTGTGCTGTAAACCACTTCACAGATTCCA 60
Qy      61  GCTTCGGAACAGAGACCCTGGTTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
Db      61  GCTTCGGAACAGAGACCCTGGTTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
Qy      121  GTTGTGACAAAAAAGACACTTATACATATGAAAAGGTTCTTTTATCTTGGCAGTAT 180
Db      121  GTTGTGACAAAAAAGACACTTATACATATGAAAAGGTTCTTTTATCTTGGCAGTAT 180
Qy      181  ATTATGACTAAACGATTATATATGATGAGAACAAACATATTTGTATTTGTTCAATGAT 240
Db      181  ATTATGACTAAACGATTATATATGATGAGAACAAACATATTTGTATTTGTTCAATGAT 240
Qy      241  CTTCTAGAGATTGTTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACACAGAAAAATATAT 300
Db      241  CTTCTAGAGATTGTTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACACAGAAAAATATAT 300
Qy      301  ACCATGATCTACAGGAACCTGTGATGATCAATCAGAGAGATCATCGGACTCGCATGATCA 360
Db      301  ACCATGATCTACAGGAACCTGTGATGATCAATCAGAGAGATCATCGGACTCGCATGATCA 360
Qy      361  TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402
Db      361  TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAT 402

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RESULT 6

ADA02668
ID ADA02668 standard; cDNA; 1476 BP.

XX ADA02668;

XX 06-NOV-2003 (first entry)

XX Human MDW2 carcinoma associated coding sequence, SEQ ID NO:1186.

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast;

XX prostate; lymphoma; leukemia; cytosolic; gene therapy; drug screening;

XX gene; ss.

XX Homo sapiens.

XX MO2003057146-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002MO-US041414.

XX 26-DEC-2001; 2001US-00035832.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-587068/55.

XX New recombinant nucleic acid encoding carcinoma associated protein,
XX PT useful for preparing compositions for treating carcinomas.

XX Claim 1; SEQ ID NO 1186; 245bp; English.

XX The invention relates to recombinant carcinoma associated (CA) nucleic
XX CC acid sequences from mouse and human (ADA01482-ADA03094), and to
XX CC recombinant carcinoma associated proteins (CAP) encoded by them. The
XX CC invention also encompasses expression vectors and host cells comprising a
XX CC CA nucleic acid, a polypeptide (especially an antibody) that specifically

CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 9; Length 1476;

Best Local Similarity 100.0%; Pred. No. 2.5e-106; Mismatches 0; Indels 0; Gaps 0;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCAATACCAACATGTCTGTACTGATGAGTGGCTGTAAACCACTCACAAGTTCCA 60

Db 1 ATGTGCAATACCAACATGTCTGTACTGATGAGTGGCTGTAAACCACTCACAAGTTCCA 60

Qy 61 GCTTCGGAACAAGAGACCCCTGTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120

Db 61 GCTTCGGAACAAGAGACCCCTGTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120

Qy 121 GTTGTGACACAAAAGACACTTATCTATGAAAAGGCTTTTATATCTGGCCAGTAT 180

Db 121 GTTGTGACACAAAAGACACTTATCTATGAAAAGGCTTTTATATCTGGCCAGTAT 180

Qy 181 ATTATGACTTAACGATTATATGATGAGAAGCAACATATGTATATTTGTTCAATATAT 240

Db 181 ATTATGACTTAACGATTATATGATGAGAAGCAACATATGTATATTTGTTCAATATAT 240

Qy 241 CTTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAAAGACAGAGAAATATAT 300

Db 241 CTTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAAAGACAGAGAAATATAT 300

Qy 301 ACCATGATCTACAGAACTTGTGTAGTATGATCAATCAGCAGAAATCATCGACTCAGTACA 360

Db 301 ACCATGATCTACAGAACTTGTGTAGTATGATCAATCAGCAGAAATCATCGACTCAGTACA 360

Qy 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

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Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

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Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

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Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

XX 02-MAR-2001; 2001US-00798586.
PR 23-OCT-2001; 2001US-00004113.
PR 08-NOV-2001; 2001US-00052482.
PR 30-NOV-2001; 2001US-00977722.
PR 20-DEC-2001; 2001US-00034650.
XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;
PI WPI; 2003-239337/23.

DR New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
XX cancers, neoplasms, adenocarcinoma, or sarcomas.

XX Claim 1; SEQ ID NO 234; 2304pp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a
XX nucleotide sequence selected from any of the 660 sequences fully defined
XX in the specification. A polynucleotide of the invention has cytoskeletal
XX activity, and may have a use in gene therapy, or in a vaccine. The
XX recombinant nucleic acids and polypeptides are useful for treating
XX carcinomas, e.g. lymphomas, cancers, neoplasms, adenocarcinoma, and
XX sarcomas. The present sequence represents a human cDNA of the invention.

XX Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 10; Length 1476;

Best Local Similarity 100.0%; Pred. No. 2.5e-106; Mismatches 0; Indels 0; Gaps 0;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCAATACCAACATGTCTGTACTGATGAGTGGCTGTAAACCACTCACAAGTTCCA 60

Db 1 ATGTGCAATACCAACATGTCTGTACTGATGAGTGGCTGTAAACCACTCACAAGTTCCA 60

Qy 61 GCTTCGGAACAAGAGACCCCTGTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120

Db 61 GCTTCGGAACAAGAGACCCCTGTAGACCAAGCCATTCTTTGAAATTAAAGTCT 120

Qy 121 GTTGTGACACAAAAGACACTTATCTATGAAAAGGCTTTTATATCTGGCCAGTAT 180

Db 121 GTTGTGACACAAAAGACACTTATCTATGAAAAGGCTTTTATATCTGGCCAGTAT 180

Qy 181 ATTATGACTTAACGATTATATGATGAGAAGCAACATATGTATATTTGTTCAATATAT 240

Db 181 ATTATGACTTAACGATTATATGATGAGAAGCAACATATGTATATTTGTTCAATATAT 240

Qy 241 CTTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAAAGACAGAGAAATATAT 300

Db 241 CTTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAAAGACAGAGAAATATAT 300

Qy 301 ACCATGATCTACAGAACTTGTGTAGTATGATCAATCAGCAGAAATCATCGACTCAGTACA 360

Db 301 ACCATGATCTACAGAACTTGTGTAGTATGATCAATCAGCAGAAATCATCGACTCAGTACA 360

Qy 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Db 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

Qy 402 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTAT 402

XX OS Homo sapiens.
XX PN W02003039484-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-US036071.
XX PR 08-NOV-2001; 2001US-00052482.
XX PA (SAGR-) SAGRES DISCOVERY.
XX PI Morris DW, Engelhard EK;
XX DR WPI; 2003-441462/41.
XX PT New carcinoma associated nucleic acids and proteins, useful for screening
XX PT drug candidates, or for diagnosing and treating carcinomas, e.g.
XX PT lymphoma, breast cancer, prostate cancer or leukemia.
XX PS Claim 1; SEQ ID NO 174; 793bp; English.
XX CC This invention relates to novel recombinant nucleic acids for use in
XX CC diagnosis and treatment of cancer, especially carcinomas, as well as the
XX CC use of compositions in screening methods. The compositions of the
XX CC invention may have cytostatic activity whilst the disclosed sequences may
XX CC be useful for gene therapy. The carcinoma associated nucleic acids and
XX CC proteins are useful for diagnosing and treating carcinomas, for example
XX CC lymphoma, breast cancer, prostate cancer or leukemia, or for screening
XX CC drug candidates or bioactive agents capable of binding to, or modulating
XX CC the activity of, a carcinoma associated protein. The present sequence is
XX CC the coding DNA sequence of the human MDM2 gene which is a carcinoma
XX CC associated gene of the invention.
SQ Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;
Query Match 100.0%; Score 402; DB 10; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2.5e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAACTTACCTCAGATTCCA 60
DB 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAACTTACCTCAGATTCCA 60
QY 61 GCTTCGGAACAGAGACCTGCTGTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 120
DB 61 GCTTCGGAACAGAGACCTGCTGTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 120
QY 121 GTTGGTGCACAAAAGACACTTATATCATATGAGAAAGGTTCTTTTATCTTGGCCAGTAT 180
DB 121 GTTGGTGCACAAAAGACACTTATATCATATGAGAAAGGTTCTTTTATCTTGGCCAGTAT 180
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACAACATTTGTTTCAATGAT 240
DB 181 ATTATGACTAAACGATTATATGATGAGAGCAACAACATTTGTTTCAATGAT 240
QY 241 CTCTAGAGAGATTGTTGGGTGCCAAGCTTCTGTGAAAGAGCAGAGAAATTTAT 300
DB 241 CTCTAGAGAGATTGTTGGGTGCCAAGCTTCTGTGAAAGAGCAGAGAAATTTAT 300
QY 301 ACCATGATCTACAGGAACCTGTTAGTAGTCATATCAGACAGGATCATGCGACTGACA 360
DB 301 ACCATGATCTACAGGAACCTGTTAGTAGTCATATCAGACAGGATCATGCGACTGACA 360
QY 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGTAT 402
DB 361 TCTGTGAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGTAT 402

RESULT 9
ADN71935
ID ADN71935 standard; cDNA; 2371 BP.

XX AC ADN71935;
XX DT 12-AUG-2004 (first entry)
XX DE MDM2 encoding cDNA SEQ ID NO:21.
XX KW kinase pathway inhibitor; anti-prostate cancer;
XX KW mitogen-activated protein kinase pathway inhibitor;
XX KW MDM2 kinase pathway inhibitor; prostate cancer inhibitor;
XX KW phosphatidylinositol 3-kinase/Akt kinase pathway;
XX KW PI3K/Akt kinase pathway; cytosolic; MAP kinase inhibitor;
XX KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
XX KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
XX KW MDM2; gene; ss.
XX OS Unidentified.
XX FH Key
XX FH Location/Qualifiers
XX FT CDS
XX FT 311..1786
XX FT /*tag= a
XX FT /product= "MDM2"
XX PN W02004041185-A2.
XX PD 21-MAY-2004.
XX PF 31-OCT-2003; 2003WO-US034636.
XX PR 31-OCT-2002; 2002US-0423340P.
XX PA (UYRP) UNIV ROCHESTER.
XX PI Chang C, Lee Y, Lin W;
XX DR WPI; 2004-390508/36.
XX DR P-PSDB; ADN71936.
XX PT Composition useful in the treatment of e.g. prostate cancer comprises a
XX PT kinase pathway inhibitor and an anti-prostate cancer compound.
XX PS Disclosure; SEQ ID NO 21; 118bp; English.
XX CC The present invention describes a composition (C1) which comprises a
XX CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
XX CC Also described: (1) identification of a mitogen-activated protein (MAP)
XX CC kinase pathway inhibitor involving incubating an antiandrogen or a
XX CC library of molecules with a cell containing an activable MAP kinase
XX CC pathway and selecting the molecules which inhibit the activation of the
XX CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
XX CC involving incubating a cell with hydroxyflutamide and potential
XX CC inhibitor, and assaying the level of activation of MAP kinase pathway or
XX CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
XX CC cytosolic activity, and can be used as a MAP kinase inhibitor,
XX CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
XX CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
XX CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
XX CC prostate cancer inhibitor; and for reducing the number of prostate cancer
XX CC cells in a sample. The composition C1 provides effective combination
XX CC therapy as compared to prior therapies. The present sequence encodes
XX CC MDM2, which is used in the exemplification of the present invention.
SQ Sequence 2371 BP; 698 A; 490 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 402; DB 12; Length 2371;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAACTTACCTCAGATTCCA 60
DB 311 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTAACTTACCTCAGATTCCA 370
QY 61 GCTTCGGAACAGAGACCTGCTGTAGACCAAGCATTGCTTTGAAGTTATTAAGTCT 120

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Db      |||
371 GCTTGGGAACAGAGACCTGGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 430
Qy      |||
121 GTTGTGACAAAAGAGACCTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGAT 180
Db      |||
431 GTTGTGACAAAAGAGACCTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGAT 490
Qy      |||
181 ATTATGACTAAACGATATATGATGAGAAGCAACACATATGATTTGTTCAATGAT 240
Db      |||
491 ATTATGACTAAACGATATATGATGAGAAGCAACACATATGATTTGTTCAATGAT 550
Qy      |||
241 CTTTAGAGAGATTGTTGGCGTGCCAAAGCTTCTGTGAAAGACACAGAAAATATAT 300
Db      |||
551 CTTTAGAGAGATTGTTGGCGTGCCAAAGCTTCTGTGAAAGACACAGAAAATATAT 610
Qy      |||
301 ACCATGATCTACAGAACTTGGTAGTACATCAATGACAGAAATCTCGACTCAGGTCA 360
Db      |||
611 ACCATGATCTACAGAACTTGGTAGTACATCAATGACAGAAATCTCGACTCAGGTCA 670
Qy      |||
361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGAAT 402
Db      |||
671 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGAAT 712

```

RESULT 10
AAQ49891
ID AAQ49891 standard; cDNA; 2372 BP.

AC AAQ49891;

DT 25-MAR-2003 (revised)
DT 05-MAY-1994 (first entry)

XX Human MDM2 gene.

XX p53 gene; tumour suppressor gene; regulation; cellular proliferation;
KW cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW gene amplification; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 312..1787
FT CDS /*tag= a
FT /product= "Human MDM2"

XX W09320238-A2.

XX 14-OCT-1993.

XX PD 07-APR-1993; 93WO-US003199.

XX PR 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX DR WPI; 1993-336944/42.

XX DR P-PSDB; AAR42175.

XX PT Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene
FT expression, also new DNA, MDM2 protein, antibodies and treatment of
PT sarcoma by inhibiting MDM2 expression.

XX PS Claim 19; Fig 1; 75pp; English.

XX This sequence represents the MDM2 gene. Amplification of this gene is
CC diagnostic of neoplasia or the potential for neoplasia. The protein
CC encoded by this gene interacts with the product of the p53 gene. p53 is a
CC tumour suppressor gene and encodes a protein which appears to be a member
CC of a group of proteins which regulate normal cellular proliferation and

CC suppression of cellular transformation. Inactivation of the p53 gene has
CC been implicated in the formation, or progression of a wide variety of
CC carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or
CC the DNA encoding these, may be used to inhibit the growth of tumour cells
CC containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      |||
1 ATGTCATATACCAATGCTGTCTACTAGTATGCTGTATACACCTCAGATTGCA 60
Db      |||
312 ATGTCATATACCAATGCTGTCTACTAGTATGCTGTATACACCTCAGATTGCA 371
Qy      |||
61 GCTTCGGAACAGAGACCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
Db      |||
372 GCTTCGGAACAGAGACCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
Qy      |||
121 GTTGTGACAAAAGAGACCTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGAT 180
Db      |||
432 GTTGTGACAAAAGAGACCTTATCTATGAAAGAGGTTCTTTTATCTTGGCCAGAT 491
Qy      |||
181 ATTATGACTAAACGATATATGATGAGAAGCAACACATATGATTTGTTCAATGAT 240
Db      |||
492 ATTATGACTAAACGATATATGATGAGAAGCAACACATATGATTTGTTCAATGAT 551
Qy      |||
241 CTTTAGAGAGATTGTTGGCGTGCCAAAGCTTCTGTGAAAGACACAGAAAATATAT 300
Db      |||
552 CTTTAGAGAGATTGTTGGCGTGCCAAAGCTTCTGTGAAAGACACAGAAAATATAT 611
Qy      |||
301 ACCATGATCTACAGAACTTGGTAGTACATCAATGACAGAAATCTCGACTCAGGTCA 360
Db      |||
612 ACCATGATCTACAGAACTTGGTAGTACATCAATGACAGAAATCTCGACTCAGGTCA 671
Qy      |||
361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGAAT 402
Db      |||
672 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGAAT 713

```

RESULT 11
AAQ94589
ID AAQ94589 standard; cDNA; 2372 BP.

XX AAQ94589;

XX 16-OCT-2003 (revised)

XX DT 01-NOV-1995 (first entry)

XX XX Human MDM2 gene.

XX KW MDM2; sarcoma; diagnostic; DNA probe; ds.

XX OS Homo sapiens; (cell line CaCo-2).

XX FH Key Location/Qualifiers
FT CDS 312..1784
FT /*tag= a

XX PN US5420263-A.

XX PD 30-MAY-1995.

XX PF 07-APR-1993; 93US-00044619.

XX PR 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Vogelstein B, Kinzler KW;

XX WPI; 1995-206312/27.
DR P-PSDB; AAR76696.
XX
PT New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
treatment of tumours.
XX
PS Claim 1; Col 19-24; 34pp; English.
XX
CC The human MDM2 gene is genetically altered (i.e. amplified) in human
tumour cells. Detecting that the gene has become amplified or detecting
increased gene product expression (using probes, proteins, antibodies and
inhibitors) allows diagnosis and therapy of cancers such as colorectal
carcinoma, lung cancer and chronic myelogenous leukaemia. The human MDM2
protein binds to human p53 and allows the cell to escape from p53-
regulated growth. (Updated on 16-Oct-2003 to standardise OS field)
CC
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCAATACCAACATGCTGTGACCTACTGATGCTGCTGTACACCTGACAGATTCCA 60
DB 312 ATGTGCAATACCAACATGCTGTGACCTACTGATGCTGCTGTACACCTGACAGATTCCA 371
QY 61 GCTTCGGACAGAGACCCCTGGTGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGACAGAGACCCCTGGTGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGACACAAAAGACACTTATATGAGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGACACAAAAGACACTTATATGAGAAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTTAACCATTTATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 240
DB 492 ATTATGACTTAACCATTTATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGAAAGAGCAGAGAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGAAAGAGCAGAGAAATATAT 611
QY 301 ACCATGATCTACAGGAACCTTGTAAGTACATCAGCAGAGATCATCGACTCAGTACA 360
DB 612 ACCATGATCTACAGGAACCTTGTAAGTACATCAGCAGAGATCATCGACTCAGTACA 671
QY 361 TCTGTGAGTGAAGACAGGTGTACCTTGAAAGTGGAGTGAT 402
DB 672 TCTGTGAGTGAAGACAGGTGTACCTTGAAAGTGGAGTGAT 713
RESULT 12
AAT45151
ID AAT45151 standard; cDNA; 2372 BP.
XX
AC AAT45151;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1997 (first entry)
XX
DE Human MDM-2 gene cDNA clone, involved in tumour-development.
XX
KM p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
KM antibody fusion protein; therapy; dr.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 312..1787
FT /+tag= a
XX
PN US5550023-A.

XX
PD 27-AUG-1996.
XX
PF 18-MAY-1994; 94US-00245500.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW;
XX
DR WPI; 1996-401591/40.
DR P-PSDB; AAW07887.
XX
PT Identification of cpds. interfering with human MDM2/p53 binding - useful
as therapeutic agents to treat human neoplastic cells.
XX
PS Example 1; Col 21-26; 36pp; English.
XX
CC AAT45151 is a cDNA clone of the human MDM-2 gene derived from a human
colon carcinoma cell line Caco-2. The MDM-2 protein produced by this
clone is used in a method for identifying compounds that interfere with
the binding of p53 and MDM-2. In binding the p53 protein, the MDM-2
protein releases a cell from p53-regulated growth, allowing cancers to
develop. Therefore compounds identified as interfering with the binding
of MDM-2 to p53 are potentially useful in the treatment of human
neoplastic cells. In the method pref. one or both of the proteins is a
fusion protein esp. with an antibody or antibody fragment which aids
separation and identification. (Updated on 25-MAR-2003 to correct PF
field.)
CC
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCAATACCAACATGCTGTGACCTACTGATGCTGCTGTACACCTGACAGATTCCA 60
DB 312 ATGTGCAATACCAACATGCTGTGACCTACTGATGCTGCTGTACACCTGACAGATTCCA 371
QY 61 GCTTCGGACAGAGACCCCTGGTGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGACAGAGACCCCTGGTGAACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
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QY 181 ATTATGACTTAACCATTTATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 240
DB 492 ATTATGACTTAACCATTTATGATGAGAGCAACAATATTGTAATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGAAAGAGCAGAGAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAGCTTCTCTGAAAGAGCAGAGAAATATAT 611
QY 301 ACCATGATCTACAGGAACCTTGTAAGTACATCAGCAGAGATCATCGACTCAGTACA 360
DB 612 ACCATGATCTACAGGAACCTTGTAAGTACATCAGCAGAGATCATCGACTCAGTACA 671
QY 361 TCTGTGAGTGAAGACAGGTGTACCTTGAAAGTGGAGTGAT 402
DB 672 TCTGTGAGTGAAGACAGGTGTACCTTGAAAGTGGAGTGAT 713
RESULT 13
AAT66410
ID AAT66410 standard; cDNA; 2372 BP.
XX
AC AAT66410;


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XX 25-MAR-2003 (revised)
DT 14-SEP-2000 (revised)
DT 18-JUN-1997 (first entry)
XX Human MDM2 coding sequence.
XX
XX Human: MDM2 protein; antibody; detection; cancer; diagnosis;
XX p53-regulated growth; db.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 312..1787
XX FT /*tag= a
XX FT /product= "MDM2"
XX
XX US5618921-A.
XX
XX PD 08-APR-1997.
XX
XX PF 17-FEB-1995; 95US-00390479.
XX
XX PR 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelestein B, Kinzler KW, Burrell M, Hill DE;
XX WPI: 1997-225474/20.
XX DR P-PSDB; AAM15463.
XX
XX PT Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
XX PS Claim 1; Col 19-24; 35pp; English.
XX
XX CC This sequence encodes the human MDM2 protein. Antibodies that
XX specifically bind to human MDM2 protein may be used for detecting
XX elevated expression of the MDM2 gene in a human tissue or body fluid
XX sample, esp. for cancer diagnosis. The antibodies may be used to
XX interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
XX to sequester p53 and allow the cell to escape from p53-regulated growth.
XX (N.B. Revised record issued to correct the sequence analysis field.)
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 402; DB 2; Length 2372;
XX Best Local Similarity 100.0%; Pred. No. 3e-106;
XX Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 ATGTGCAATACCAACATGTCTGTACTCTACTGATGCTGTAAACCACTCACAAGATTCCA 60
XX |||||||
XX DB 312 ATGTGCAATACCAACATGTCTGTACTCTACTGATGCTGTAAACCACTCACAAGATTCCA 371
XX
XX QY 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTCTTTGAAGTTATTAAGTCT 120
XX |||||||
XX DB 372 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTCTTTGAAGTTATTAAGTCT 431
XX
XX QY 121 GTTGTGACAAAAAGACACTTATCTATGAAAGGCTTTTATCTTGGCCAGTAT 180
XX |||||||
XX DB 432 GTTGTGACAAAAAGACACTTATCTATGAAAGGCTTTTATCTTGGCCAGTAT 491
XX
XX QY 181 ATTATGACTAATACGATTTATGATGAGAAGCAACAATATTGTATTGTTCAATGAT 240
XX |||||||
XX DB 492 ATTATGACTAATACGATTTATGATGAGAAGCAACAATATTGTATTGTTCAATGAT 551
XX
XX QY 241 CTTTAGAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGACACAGAAAATATAT 300
XX |||||||
XX DB 552 CTTTAGAGAGATTGTTGGCGTGCAGAGCTTCTGTGAAAGACACAGAAAATATAT 611
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QY 301 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGAAATCATCGACTCAGATACA 360
XX |||||||
XX DB 612 ACCATGATCTACAGAACTTGTAAGTCAATCAGCAGAAATCATCGACTCAGATACA 671
XX
XX QY 361 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGGTGGAGTGAT 402
XX |||||||
XX DB 672 TCTGTGAGTGAGAAACAGGTGTCACTTGAAGGTGGAGTGAT 713
XX
XX RESULT 14
XX AAT62065
XX ID AAT62065 standard; cDNA; 2372 BP.
XX
XX AC AAT62065;
XX
XX DT 25-MAR-2003 (revised)
XX DT 05-JUN-1997 (first entry)
XX
XX DE Human MDM2 cDNA.
XX
XX XX Human: MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
XX elevation; expression; diagnosis; neoplasia; neoplastic transformation;
XX sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia; db.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT 312..1787
XX FT /*tag= a
XX FT /product= "MDM2"
XX
XX XX US5606044-A.
XX
XX PN 25-FEB-1997.
XX
XX PD 17-FEB-1995; 95US-00390546.
XX
XX PF 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Kinzler KW, Vogelestein B, Hill DE, Burrell M;
XX WPI: 1997-153623/14.
XX DR P-PSDB; AAM13380.
XX
XX PT Detection of amplification of human MDM2 gene - useful for diagnosis of
XX neoplasia or potential neoplastic transformation.
XX
XX PS Claim 1; Col 21-24; 35pp; English.
XX
XX CC The present sequence is the human MDM2 cDNA, which was isolated from a
XX human CaCo-2 colonic carcinoma cell cDNA library using a murine MDM2 cDNA
XX probe. The MDM2 cDNA can be used as a probe to detect the amplification
XX or elevated expression of a human MDM2 gene, which is diagnostic of
XX neoplasia or the potential for neoplastic transformation, useful for the
XX detection of, e.g. sarcomas, colorectal carcinoma, lung cancer and
XX chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to correct PF
XX field.)
XX
XX SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 402; DB 2; Length 2372;
XX Best Local Similarity 100.0%; Pred. No. 3e-106;
XX Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ATGTGCAATACCAACATGTCTGTACTCTACTGATGCTGTAAACCACTCACAAGATTCCA 60
XX |||||||
XX DB 312 ATGTGCAATACCAACATGTCTGTACTCTACTGATGCTGTAAACCACTCACAAGATTCCA 371
XX
XX QY 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTCTTTGAAGTTATTAAGTCT 120
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2004, 11:45:45 ; Search time 374 Seconds

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Scoring table: IDENTITY_NUC

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	402	100.0	2372	1	US-08-283-911-1
6	402	100.0	2372	1	US-08-245-500A-2
7	402	100.0	2372	1	US-08-390-546-2
8	402	100.0	2372	1	US-08-390-479A-2
9	402	100.0	2372	1	US-08-557-393-2
10	402	100.0	2372	1	US-08-390-516C-2
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14	402	100.0	2372	3	US-09-073-567-1
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16	402	100.0	2372	3	US-09-048-810-1
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21	289.2	71.9	1710	1	US-08-283-911-3
22	289.2	71.9	1710	1	US-08-245-500A-4
23	289.2	71.9	1710	1	US-08-390-546-4
24	289.2	71.9	1710	1	US-08-390-479A-4
25	289.2	71.9	1710	1	US-08-557-393-4
26	289.2	71.9	1710	1	US-08-390-516C-4
27	289.2	71.9	1710	1	US-08-390-517A-4

28	289.2	71.9	1710	1	US-08-390-515A-4	Sequence 4, Appli
29	289.2	71.9	1710	2	US-08-801-718-4	Sequence 4, Appli
30	289.2	71.9	1710	3	US-09-073-567-12	Sequence 12, Appli
31	289.2	71.9	1710	3	US-09-170-159A-4	Sequence 4, Appli
32	289.2	71.9	1710	4	US-09-480-718-45	Sequence 45, Appli
33	289.2	56.5	309	3	US-09-167-322-9	Sequence 9, Appli
34	160.8	40.0	966	3	US-09-167-322-7	Sequence 7, Appli
35	131	32.6	199	4	US-09-200-355-1	Sequence 1, Appli
36	131	32.6	199	4	US-09-200-355-2	Sequence 2, Appli
37	95.6	23.8	2192	3	US-09-289-267-1	Sequence 1, Appli
38	88.8	22.1	3399	3	US-09-167-322-8	Sequence 8, Appli
39	82.4	20.5	891	3	US-09-167-322-5	Sequence 5, Appli
40	82	20.4	657	3	US-09-167-322-6	Sequence 6, Appli
41	70.8	17.6	500	3	US-09-280-805-2	Sequence 2, Appli
42	70.8	17.6	500	3	US-09-048-810-2	Sequence 2, Appli
43	49	12.2	73	3	US-09-073-567-49	Sequence 49, Appli
44	38.4	9.6	40	3	US-09-540-699-17	Sequence 17, Appli
45	36.8	9.2	399	4	US-09-621-976-8976	Sequence 8976, Ap

ALIGNMENTS

```
RESULT 1
US-09-510-252-3
: Sequence 3, Application US/09510252
: Patent No. 6372490
: GENERAL INFORMATION:
: APPLICANT: Nandabalan, Krishnan
: APPLICANT: Yang, Meljia
: APPLICANT: Schulz, Vincent
: APPLICANT: Curagen Corporation
: TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
: FILE REFERENCE: 15966-524 MDM US
: CURRENT APPLICATION NUMBER: 2000-02-22
: PRIOR FILING DATE: 1999-02-23
: PRIOR APPLICATION NUMBER: USSN 60/121,192
: PRIOR FILING DATE: 1999-03-03
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 3
: LENGTH: 652
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-510-252-3

Query Match          100.0%; Score 402; DB 3; Length 652;
Best Local Similarity 100.0%; Pred. No. 2, 3e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACACCTCAGACATTCCA 60
DB      1 ATGTGCAATACCAACATGTCTGTACTGATGATGCTGTAAACACCTCAGACATTCCA 60

QY      61 GCTTCGGAACAGAGACCCCTGCTTAAAGCAAGGCATTGCTTTGAAGTTATTTAAAGTCT 120
DB      61 GCTTCGGAACAGAGACCCCTGCTTAAAGCAAGGCATTGCTTTGAAGTTATTTAAAGTCT 120

QY      121 GTTGGTGCACAAAAGACCTTATCTATGATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB      121 GTTGGTGCACAAAAGACCTTATCTATGATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180

QY      181 ATTATGACTTAAAGCATTTATATGATGAGAACCAACATATTGTATATTGTTCAATGAT 240
DB      181 ATTATGACTTAAAGCATTTATATGATGAGAACCAACATATTGTATATTGTTCAATGAT 240

QY      241 CTTCTAGAGATTGTTGTCGCGCCCAAGCTTCTCTGTGAAAGCAGAGAAATATAT 300
DB      241 CTTCTAGAGATTGTTGTCGCGCCCAAGCTTCTCTGTGAAAGCAGAGAAATATAT 300

QY      301 ACATGATCTACAGGAAGTGTAGTAGTCAATCAGAGAAATCATCGACTCAGTACA 360
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Db 301 ACCATGATCTACAGAACTTGTGTAGTACTAATCAGACAGAAATATCGAGTCAAGTACA 360
QY 361 TCTGTGAGTGAGAACAGAGTGTCACTTGAAGGTGGAGTGTAT 402
Db 361 TCTGTGAGTGAGAACAGAGTGTCACTTGAAGGTGGAGTGTAT 402

RESULT 2
US-09-603-052-3

; Sequence 3, Application US/09603052
; Patent No. 6492116
; GENERAL INFORMATION:
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
; TITLE OF INVENTION: between proteins p53 and dm2
; FILE REFERENCE: MEMB26.001C1
; CURRENT APPLICATION NUMBER: US/09/603,052
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: EP 95810576.9
; PRIOR FILING DATE: 1995-09-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03957
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)..(650)
; OTHER INFORMATION: N-terminal 188 amino acids of human double minute
; OTHER INFORMATION: protein 2
US-09-603-052-3

Query Match 100.0%; Score 402; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 2,4e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTTACTGATGTGTCTGTAAACCACTCAGATTTCCA 60
Db 84 ATGTGCAATACCAACATGTCTGTACTTACTGATGTGTCTGTAAACCACTCAGATTTCCA 143
QY 61 GCTTCGGAACAGAGCCCTGTGTAGACCAAAAGCATTGCTTTGAAGTATTAAAGTCT 120
Db 144 GCTTCGGAACAGAGCCCTGTGTAGACCAAAAGCATTGCTTTGAAGTATTAAAGTCT 203
QY 121 GTTGTGACACAAAAGACACTTATATCTATGAAAGAGTCTTTTATCTTGGCCAGTAT 180
Db 204 GTTGTGACACAAAAGACACTTATATCTATGAAAGAGTCTTTTATCTTGGCCAGTAT 263
QY 181 ATTATGACTTAACGATTATATGATGAGAGCAACAATATTTGTTCAATGAT 240
Db 264 ATTATGACTTAACGATTATATGATGAGAGCAACAATATTTGTTCAATGAT 323
QY 241 CTTCTAGAGATTGTTGGGTGCCAAGCTTCTCTGTGAAAGAGCAAGAGAAATATAT 300
Db 324 CTTCTAGAGATTGTTGGGTGCCAAGCTTCTCTGTGAAAGAGCAAGAGAAATATAT 383
QY 301 ACCATGATCTACAGAACTTGTGTAGTACTAATCAGACAGAAATATCGAGTCAAGTACA 360
Db 384 ACCATGATCTACAGAACTTGTGTAGTACTAATCAGACAGAAATATCGAGTCAAGTACA 443
QY 361 TCTGTGAGTGAGAACAGAGTGTCACTTGAAGGTGGAGTGTAT 402
Db 444 TCTGTGAGTGAGAACAGAGTGTCACTTGAAGGTGGAGTGTAT 485

RESULT 3
US-07-903-103-1
; Sequence 1, Application US/07903103

; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107,40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMBB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: Caco-2
; POSITION IN GENOME:
; MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
US-07-903-103-1

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3,5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTTACTGATGTGTCTGTAAACCACTCAGATTTCCA 60
Db 312 ATGTGCAATACCAACATGTCTGTACTTACTGATGTGTCTGTAAACCACTCAGATTTCCA 371
QY 61 GCTTCGGAACAGAGCCCTGTGTAGACCAAAAGCATTGCTTTGAAGTATTAAAGTCT 120
Db 372 GCTTCGGAACAGAGCCCTGTGTAGACCAAAAGCATTGCTTTGAAGTATTAAAGTCT 431
QY 121 GTTGTGACACAAAAGACACTTATATCTATGAAAGAGTCTTTTATCTTGGCCAGTAT 180
Db 432 GTTGTGACACAAAAGACACTTATATCTATGAAAGAGTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTTAACGATTATATGATGAGAGCAACAATATTTGTTCAATGAT 240
Db 492 ATTATGACTTAACGATTATATGATGAGAGCAACAATATTTGTTCAATGAT 551

Qy 241 CTTGATGAGATTTGTTGGCGTCCAGCTTCTGTGAAAGACACAGAAAAATATAT 300
 Db 552 CTTGATGAGATTTGTTGGCGTCCAGCTTCTGTGAAAGACACAGAAAAATATAT 611
 Qy 301 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 360
 Db 612 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 671
 Qy 361 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGTAT 402
 Db 672 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGTAT 713

RESULT 4
 US-08-044-619A-1
 ; Sequence 1, Application US/0804619A
 ; Patent No. 5420263
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
 ; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G ST., N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001-4597

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/044,619A
 FILING DATE: 07-APR-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/903,103
 FILING DATE: 23-JUN-1992
 APPLICATION NUMBER: US 07/867,840
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107,40148
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 197430 BBMB UT
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL LINE: CaCo-2
 POSITION IN GENOME:
 MAP POSITION: 12q12-14
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 312..1784
 US-08-044-619A-1

Query Match 100.0%; Score 402; DB 1; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3,5e-103;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGTGCAATACCAACATGCTGTACCTTACATGATGCTGCTTAACCACTCAGATTC 60
 Db 312 ATGTGCAATACCAACATGCTGTACCTTACATGATGCTGCTTAACCACTCAGATTC 371
 Qy 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAAAGCATTTGTTGAATTAATTAAGTCT 120
 Db 372 GCTTCGGAACAAGAGACCCCTGTTAGACCAAAAGCATTTGTTGAATTAATTAAGTCT 431
 Qy 121 GTTGTGCACAAAAAGACCTTATATATGAGAAAGAGGTTCTTTTATCTTGGCCAGTAT 180
 Db 432 GTTGTGCACAAAAAGACCTTATATATGAGAAAGAGGTTCTTTTATCTTGGCCAGTAT 491
 Qy 181 ATTTGACTAAACGATTTATATGATGAGAACCAACATATTTGATTTGTTCAAAATGAT 240
 Db 492 ATTTGACTAAACGATTTATATGAGAACCAACATATTTGATTTGTTCAAAATGAT 551
 Qy 241 CTTGATGAGATTTGTTGGCGTCCAGCTTCTGTGAAAGACACAGAAAAATATAT 300
 Db 552 CTTGATGAGATTTGTTGGCGTCCAGCTTCTGTGAAAGACACAGAAAAATATAT 611
 Qy 301 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 360
 Db 612 ACCATGATCTACAGAACTTGTAGTACTCAATCAGCAGAAATCAGACTCAGTACA 671
 Qy 361 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGTAT 402
 Db 672 TCTGTGATGAGAACAGGTGTCACTTGAAGTGGAGTAT 713

RESULT 5
 US-08-283-911-1
 ; Sequence 1, Application US/08283911
 ; Patent No. 5519118
 ; GENERAL INFORMATION:
 ; APPLICANT: VOGELSTEIN, BERT
 ; APPLICANT: KINZLER, KENNETH
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G ST., N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001-4597

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/283,911
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/903,103
 FILING DATE: 23-JUN-1992
 APPLICATION NUMBER: US 07/867,840
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107,40148
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 197430 BBMB UT
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs

Query Match 100.0%; Score 402; DB 1; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3,5e-103;

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-283-911-1

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAATGCTGTCTGCTACTGATGCTGTGTAACCACTCAGATTCCA 60
DB 312 ATGTGCAATACCAATGCTGTCTGCTACTGATGCTGTGTAACCACTCAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGTCACAAAAGACCTTATCTATGTAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGTCACAAAAGACCTTATCTATGTAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTTGTTCAATGAT 240
DB 492 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACAAGAAAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACAAGAAAAATATAT 611
QY 301 ACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGAAATCATGGACTCGATACA 360
DB 612 ACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGAAATCATGGACTCGATACA 671
QY 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGTAT 402
DB 672 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGTAT 713

RESULT 6
US-08-245-500A-2

Sequence 2, Application US/08245500A
Patent No. 5550023
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,500A
FILING DATE: 07-Apr-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-245-500A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAATGCTGTCTGCTACTGATGCTGTGTAACCACTCAGATTCCA 60
DB 312 ATGTGCAATACCAATGCTGTCTGCTACTGATGCTGTGTAACCACTCAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCTGCTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGTCACAAAAGACCTTATCTATGTAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGTCACAAAAGACCTTATCTATGTAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTTGTTCAATGAT 240
DB 492 ATTATGACTAAACGATTATATGATGAGAGCAACATATTGTATTTGTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACAAGAAAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAAGACAAGAAAAATATAT 611
QY 301 ACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGAAATCATGGACTCGATACA 360
DB 612 ACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGAAATCATGGACTCGATACA 671
QY 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGTAT 402
DB 672 TCTGTGAGTGAAGACAGGTGTCACTTGAAGGTGGAGTGTAT 713

RESULT 7

US-08-390-546-2
Sequence 2, Application US/08390546
Patent No. 5606044
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDK2 GENE IN
NUMBER OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,546
FILING DATE: 07-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-546-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGCTGTACCTAATGATGGTGTGAACCACTCAAGATTCCA 60
DB 312 ATGTGCAATACCAACATGCTGTACCTAATGATGGTGTGAACCACTCAAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCACTGTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCACTGTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGACAAAAGACACTTATATCTATGAAGAGTCTCTTTTATCTTGGCAGTAT 180
DB 432 GTTGTGACAAAAGACACTTATATCTATGAAGAGTCTCTTTTATCTTGGCAGTAT 491
QY 181 ATTATGACTAAAGCATTTATATGATGAGAAACAACATATTGTTTCAATGAT 240
DB 492 ATTATGACTAAAGCATTTATATGATGAGAAACAACATATTGTTTCAATGAT 551
QY 241 CTTTAGAGAGATTGTTGGGTCGCAAGCTTCTGTGGAAGAGCAAGAAAATATAT 300
DB 552 CTTTAGAGAGATTGTTGGGTCGCAAGCTTCTGTGGAAGAGCAAGAAAATATAT 611
QY 301 ACCATGATCTACAGAACTTGTGTAGTAGTCAATGACAGAAATCATCGACTCAGTACA 360
DB 612 ACCATGATCTACAGAACTTGTGTAGTAGTCAATGACAGAAATCATCGACTCAGTACA 671

QY 361 TCTGTAGTGAAGACAGGTGTACCTTGAAGTGGAGTGT 402
DB 672 TCTGTAGTGAAGACAGGTGTACCTTGAAGTGGAGTGT 713

RESULT 8
US-08-390-479A-2
Sequence 2, Application US/08390479A
Patent No. 5618921
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDK2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,479A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.48992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-479A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 312 ATGTGCAATACCAACATGCTGTACCTAATGATGGTGTGAACCACTCAAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCACTGTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCCTGTTAGACCAAGCACTGTTGAAGTTATTAAGTCT 431

QY 121 GTTGGTCACAAAAAGCACTTATCTATGAGAGAGGTTCTTTTATCTTGGCCAGTAT 180
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Db 432 GTTGGTCACAAAAAGCACTTATCTATGAGAGAGGTTCTTTTATCTTGGCCAGTAT 491
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QY 181 ATTATGACTAAAGATATATATGATGAGAGCAACAATATGATTTGTTCAAAATGAT 240
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Db 492 ATTATGACTAAAGATATATATGATGAGAGCAACAATATGATTTGTTCAAAATGAT 551
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QY 241 CTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
| | | | |
Db 552 CTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 611
| | | | |
QY 301 ACCATGATCTACAGAACTTGTTGTTGATGATCATGACAGAGATATGAGTCAAGTACA 360
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Db 612 ACCATGATCTACAGAACTTGTTGTTGATGATCATGACAGAGATATGAGTCAAGTACA 671
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QY 361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 402
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Db 672 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 713
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RESULT 9

US-08-557-393-2
; Sequence 2, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,500
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A. 32,141
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: Caco-2
; POSITION IN GENOME:

MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
US-08-557-393-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATCCCAACATGCTGTACCTACGATGAGTGGTGTACCACTTCACAGATTCCA 60
| | | | |
Db 312 ATGTGCAATCCCAACATGCTGTACCTACGATGAGTGGTGTACCACTTCACAGATTCCA 371
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QY 61 GCTTGGCAACAGAGACCCTGTGTTAGACCAAGCCATTGCTTTGAAGTATTTAAAGTCT 120
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QY 181 ATTATGACTAAAGATATATATGATGAGAGCAACAATATGATTTGTTCAAAATGAT 240
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QY 241 CTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 300
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Db 552 CTCTAGAGATTTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAATATAT 611
| | | | |
QY 301 ACCATGATCTACAGAACTTGTTGTTGATGATCATGACAGAGATATGAGTCAAGTACA 360
| | | | |
Db 612 ACCATGATCTACAGAACTTGTTGTTGATGATCATGACAGAGATATGAGTCAAGTACA 671
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Db 672 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 713
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RESULT 10

US-08-390-516C-2
; Sequence 2, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A. 32,141
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100

TELEFAX: 202-508-9239
TELEX: 197430 BMWB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-516C-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTGTAACCACTTCACAGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACTGATGCTGTGTAACCACTTCACAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGACACAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGACACAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAGCATTATATGATGAGAAAGCAACATATTTGTAATTTGTTCAAAATGAT 240
DB 492 ATTATGACTAAGCATTATATGATGAGAAAGCAACATATTTGTAATTTGTTCAAAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAAATATAT 611
QY 301 ACCATGATCTACAGGAACCTTGTAGTAGTCAATCAGCAGAAATCATCGGACTCAGGTACA 360
DB 612 ACCATGATCTACAGGAACCTTGTAGTAGTCAATCAGCAGAAATCATCGGACTCAGGTACA 671
QY 361 TCTGTGAGTAGAAGACAGGTGTCACTTGGAAGTGGAGTAT 402
DB 672 TCTGTGAGTAGAAGACAGGTGTCACTTGGAAGTGGAGTAT 713

RESULT 11
US-08-390-517A-2
Sequence 2, Application US/08390517A
Patent No. 5736338
GENERAL INFORMATION:
APPLICANT: BURELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,517A
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9239
TELEX: 197430 BMWB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-517A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTGTAACCACTTCACAGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACTGATGCTGTGTAACCACTTCACAGATTCCA 371
QY 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 372 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 431
QY 121 GTTGTGACACAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 180
DB 432 GTTGTGACACAAAAGACACTTATCTATGAAAGAGTTCTTTTATCTTGGCCAGTAT 491
QY 181 ATTATGACTAAGCATTATATGATGAGAAAGCAACATATTTGTAATTTGTTCAAAATGAT 240
DB 492 ATTATGACTAAGCATTATATGATGAGAAAGCAACATATTTGTAATTTGTTCAAAATGAT 551
QY 241 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAAATATAT 300
DB 552 CTTCTAGAGATTGTTGGCGTCCAAAGCTTCTCTGTGAAGAGCAGAGAAAATATAT 611
QY 301 ACCATGATCTACAGGAACCTTGTAGTAGTCAATCAGCAGAAATCATCGGACTCAGGTACA 360
DB 612 ACCATGATCTACAGGAACCTTGTAGTAGTCAATCAGCAGAAATCATCGGACTCAGGTACA 671
QY 361 TCTGTGAGTAGAAGACAGGTGTCACTTGGAAGTGGAGTAT 402
DB 672 TCTGTGAGTAGAAGACAGGTGTCACTTGGAAGTGGAGTAT 713

RESULT 12
US-08-390-515A-2
Sequence 2, Application US/08390515A
Patent No. 5756455

GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: HUMAN TUMORS
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,515A
FILING DATE: 07-APR-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-515A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No.3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTGATGCTGTGAACACCTCAGATTCCA 60
DB 312 ATGTGCAATACCAACATGTCTGTACTGATGCTGTGAACACCTCAGATTCCA 371
QY 61 GCTTGGCAACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTAAATGCT 120
DB 372 GCTTGGCAACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTAAATGCT 431
QY 121 GTTGGTGCACAAAAGACACTTATATGATGAGAAAGGTTCTTTTATCTTGGCAGTAT 180
DB 432 GTTGGTGCACAAAAGACACTTATATGATGAGAAAGGTTCTTTTATCTTGGCAGTAT 491
QY 181 ATTATGACTAAGCATTATATGATGAGAAAGCAACATATTTGATTTCAATGAT 240
DB 492 ATTATGACTAAGCATTATATGATGAGAAAGCAACATATTTGATTTCAATGAT 551
QY 241 CTTCTAGAGATTGTTGGGTGCGCAAGCTTCTCTGTAAAGAGCACAGAAAATATAT 300

DB 552 CTTCTAGAGATTGTTGGGTGCGCAAGCTTCTCTGTAAAGAGCACAGAAAATATAT 611
QY 301 ACCATGATCTACAGAACTGTAGTATCATCAGAGAAATCATCGACTCAGGTACA 360
DB 612 ACCATGATCTACAGAACTGTAGTATCATCAGAGAAATCATCGACTCAGGTACA 671
QY 361 TCTGTAGTGAAGAACGGTGTCACTTTGAAGGTGGAGTGTAT 402
DB 672 TCTGTAGTGAAGAACGGTGTCACTTTGAAGGTGGAGTGTAT 713

RESULT 13

US-08-801-718-2
Sequence 2, Application US/08801718
Patent No. 5858976

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,718
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/390,515
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-801-718-2

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No.3.5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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(without alignments)
1998.468 Million cell updates/sec

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Searched: 32822875 segs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: gb_est2: *
3: gb_hcc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g861: *
9: gb_g862: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	347.6	86.5	728	7	CO738288
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10	324	80.6	393	1	AL704062
11	318	79.1	518	1	AL902188
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15	294.6	73.3	512	2	BF435134
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ALIGNMENTS

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LOCUS
DEFINITION
AGENCOURT 6418503 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502336
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BM479400.1 GI:18528442
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 970)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM12140 row: 6 column: 01
High quality sequence stop: 597.
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/clone="IMAGE:5502336"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

FEATURES

source

ORIGIN

Query Match 100.0%; Score 402; DB 4; Length 970;
Best Local Similarity 100.0%; Pred. No. 3.7e-101; Indels 0; Gaps 0;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 76 ATGCGAATACCAACATGTCTGTACTGATGCTGTGTAACCACTCAGATTCACA 135
|||
Qy 61 GCTTCGGAACAGAGACCCCTGTAGACCAAGCATCTGTTTGAAGTATTAATCT 120
|||
Db 136 GCTTCGGAACAGAGACCCCTGTAGACCAAGCATCTGTTTGAAGTATTAATCT 195
|||
Qy 121 GTTGTCACAAAAAGACCTTATCATATGAGAGAGTTCTTTTATCTTGGCCAGTAT 180
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Db 196 GTTGTCACAAAAAGACCTTATCATATGAGAGAGTTCTTTTATCTTGGCCAGTAT 255
|||
Qy 181 ATTATGACTAAAGATTATATGATGAGAGCAACAATATTGTATATTGTTCAATGAT 240
|||
Db 256 ATTATGACTAAAGATTATATGATGAGAGCAACAATATTGTATATTGTTCAATGAT 315
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Qy 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGAAAGAGCAGAGAAATATAT 300
|||
Db 316 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGAAAGAGCAGAGAAATATAT 375
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Qy 301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGATCATCGACTCAGTACA 360
|||
Db 376 ACCATGATCTACAGAACTTGTAGTATGATCAGAGATCATCGACTCAGTACA 435
|||
Qy 361 TCTGTAGTGAGAAACAGGTGTACCTTGAAGTGAGATGAT 402
|||
Db 436 TCTGTAGTGAGAAACAGGTGTACCTTGAAGTGAGATGAT 477

```

RESULT 2
BF057574 709 bp mRNA linear EST 16-OCT-2000
LOCUS 744607.x1 NCI CGAP OV18 Homo sapiens cDNA clone IMAGE:3478285 3'
DEFINITION similar to SW:MDM2_HUMAN Q00987 MDM2 PROTEIN ; mRNA sequence.
ACCESSION BF057574
VERSION BF057574.1 GI:10811470
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 709) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 481.

FEATURES
source Location/Qualifiers

1..709

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3478285"
/issue_type="fibroheoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NCI_CGAP_OV18"
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGAGGAGCGCGGCAGATTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library

ORIGIN

Query Match 99.8%; Score 401; DB 2; Length 709;
Best Local Similarity 99.8%; Pred. No. 6; 5e-101;
Matches 401; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 ATGCGAATACCAACATGTCTGTACTGATGCTGTGTAACCACTCAGATTCACA 60
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Db 206 ATGCGAATACCAACATGTCTGTACTGATGCTGTGTAACCACTCAGATTCACA 255
|||
Qy 61 GCTTCGGAACAGAGACCCCTGTAGACCAAGCATCTGTTTGAAGTATTAATCT 120
|||
Db 266 GCTTCGGAACAGAGACCCCTGTAGACCAAGCATCTGTTTGAAGTATTAATCT 325
|||
Qy 121 GTTGTCACAAAAAGACCTTATCATATGAGAGAGTTCTTTTATCTTGGCCAGTAT 180
|||
Db 326 GTTGTCACAAAAAGACCTTATCATATGAGAGAGTTCTTTTATCTTGGCCAGTAT 385
|||
Qy 181 ATTATGACTAAAGATTATATGATGAGAGCAACAATATTGTATATTGTTCAATGAT 240
|||
Db 386 ATTATGACTAAAGATTATATGATGAGAGCAACAATATTGTATATTGTTCAATGAT 445
|||
Qy 241 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGAAAGAGCAGAGAAATATAT 300
|||
Db 446 CTCTAGAGATTGTTGGCGGCCAAGCTTCTCTGAAAGAGCAGAGAAATATAT 505
|||
Qy 301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGATCATCGACTCAGTACA 360
|||
Db 506 ACCATGATCTACAGAACTTGTAGTATGATCAGAGATCATCGACTCAGTACA 565
|||
Qy 361 TCTGTAGTGAGAAACAGGTGTACCTTGAAGTGAGATGAT 402
|||
Db 566 TCTGTAGTGAGAAACAGGTGTACCTTGAAGTGAGATGAT 607

```

RESULT 3

CR629819 739 bp mRNA linear EST 11-AUG-2004
LOCUS DKFZp469A1622.F1 469 (synonym: pkidi) Pongo pygmaeus cDNA clone
DEFINITION DKFZp469A1622 5', mRNA sequence.
ACCESSION CR629819
VERSION CR629819.1 GI:51125899
KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus

REFERENCE 1 (bases 1 to 739) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
AUTHORS Bahr, A., Lauber, J., Mewes, H.W., Weill, B., Amd, C., Oesanger, A.,
Pohl, G., Han, M., and Wiemann, S.
Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS

TITLE

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
(Hilden, Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp469A1622) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp469A1622>
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source Location/Qualifiers

1..739

/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469A1622"

ORIGIN

/cissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiIa; Site_2: SfiIb"

Query Match 98.2%; Score 394.6; DB 7; Length 739;
Best Local Similarity 98.8%; Pred. No. 4e-99; Mismatches 5; Indels 0; Gaps 0;
Matches 397; Conservative 0;

QY 1 ATGTGCAATACCAACATGTCTGTACCTACTGATGGTGTACACCTCCACAGATTCCA 60
DB 327 ATGTGCAATACCAACATGTCTGTACCTACTGATGGTGTACACCTCCACAGATTCCA 386
QY 61 GCTTCGGAACAAGACCCCTGGTTAGACCAAGCCATGCTTTGAGATTAAAGTCT 120
DB 387 GCTTCGGAACAAGACCCCTGGTTAGACCAAGCCATGCTTTGAGATTAAAGTCT 446
QY 121 GTTGTGACAAAAGACCTTATCTATGAAAGAGTCTTTTATCTGGCCAGTAT 180
DB 447 GTTGTGACAAAAGACCTTATCTATGAAAGAGTCTTTTATCTGGCCAGTAT 506
QY 181 ATTATGACTAAACGATTATATGATGAGAACACACATATTGTATATTTCAATGAT 240
DB 507 ATTATGACTAAACGATTATATGATGAGAACACACATATTGTATATTTCAATGAT 566
QY 241 CTTCTAGAGATTGTTGGGCTGCAAGCTTCTCTGTGAAAGACACAGAAAATATAT 300
DB 567 CTTCTAGAGATTGTTGGGCTGCAAGCTTCTCTGTGAAAGACACAGAAAATATAT 626
QY 301 ACCATGATCTACAGAACTTGTAGTACTCAATCAGAGAAATCATGGAGTCCAGTACA 360
DB 627 ACCATGATCTACAGAACTTGTAGTACTCAATCAGAGAAATCATGGAGTCCAGTACA 686
QY 361 TCTGTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTAT 402
DB 687 TCTGTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTAT 728

RESULT 4
R80343/c 482 bp mRNA linear EST 09-JUN-1995
LOCUS y196d02.r1 Soares Placenta NB2HP Homo sapiens cDNA clone
DEFINITION IMAGE:147075 5' similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA
sequence.

ACCESSION R80343
VERSION R80343.1 GI:856624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 482)
Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,D., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaekis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The Mashu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence stops: 371
Source: IMAGE Consortium, LMLN
This clone is available royalty-free through LMLN; contact the
IMAGE Consortium (info@image.lmln.gov) for further information.
Insert Length: 529 Std Error: 0.00

Seq primer: M13RP1
High quality sequence stop: 371.
Location/Qualifiers
1..482

FEATURES

Source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:558688"
/db_xref="taxon:9606"
/clone="IMAGE:147075"
/sex="Female"
/dev_stage="Placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares Placenta NB2HP"
/note="Organ: placenta; Vector: p773D (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AAGTCGAGAAATTCGCGCGCAGAGAAATTTTATTTTATTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 92.9%; Score 373.4; DB 7; Length 482;
Best Local Similarity 99.2%; Pred. No. 3e-93; Mismatches 1; Indels 2; Gaps 2;
Matches 396; Conservative 0;

QY 6 CAATACCAACATGTCTGTACTACTGATGCTG-CTGTACCACTCAAGATT-CCAGCT 63
DB 421 CAATACCAACATGTCTGTACTACTGATGCTGCTGTACCACTCAAGATTCCAGCT 362
QY 64 TCGGAACAAGACCCCTGGTTAGACCAAGCCATGCTTTGAGATTAAATCTGTT 123
DB 361 TCGGAACAAGACCCCTGGTTAGACCAAGCCATGCTTTGAGATTAAATCTGTT 302
QY 124 GGTGCAAAAAGACCTTATCTATGAAAGAGTCTTTTATCTTGGCCAGTATAT 183
DB 301 GGTGCAAAAAGACCTTATCTATGAAAGAGTCTTTTATCTTGGCCAGTATAT 242
QY 184 ATGACTTAACGATTATATGATGAGAACCAACATATTGTATTTGTCATATGATCTT 243
DB 241 ATGACTTAACGATTATATGATGAGAACCAACATATTGTATTTGTCATATGATCTT 182
QY 244 CTAGAGATTGTTGGCGGCCCAAGCTTCTCTGTGAAAGACACAGAAAATATATACC 303
DB 181 CTAGAGATTGTTGGCGGCCCAAGCTTCTCTGTGAAAGACACAGAAAATATATACC 122
QY 304 ATGATCTACAGAACTTGTAGTACTCAATCAGAGAAATCATGAGTCCAGTACATCT 363
DB 121 ATGATCTACAGAACTTGTAGTACTCAATCAGAGAAATCATGAGTCCAGTACATCT 62
QY 364 GTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTAT 402
DB 61 GTGAGTGAAGACAGGTGTACCTTGAGAGTGGAGTAT 23

RESULT 5
LOCUS CO737650
DEFINITION CO737650 779 bp mRNA linear EST 29-JUL-2004
SIH03C18d24f1 squirrel heart library 1 Sperophilus lateralis cDNA
clone 18d24 5', mRNA sequence.

ACCESSION CO737650
VERSION CO737650.1 GI:50824920
KEYWORDS EST.
SOURCE Sperophilus lateralis (golden-mantled ground squirrel)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
Sperophilus.

REFERENCE
AUTHORS 1 (bases 1 to 779)
Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
Rogers,J. and Cosvine,A.R.

TITLE Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, *Spermophilus lateralis*
JOURNAL Unpublished (2004)
COMMENT Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 18 row: d column: 24
Seq primer: pf1c t7 (5'-AATACGACTCACTATAGG-3')
High quality sequence stop: 779.
Location/Qualifiers

FEATURES

source 1..779
/organism="Spermophilus lateralis"
/mol_type="mRNA"
/db_xref="taxon:76772"
/clone="18d24"
/sex="Male & female"
/tissue_type="Heart"
/dev_stage="Adult"
/lab_host="E.coli Electromax DH10B"
/clone_1b="squirrel heart library 1"
/note="Vector: pFLC; Site 1: Sail GTCGAG; Site 2: BamHI GCATCC; Normalized and subcloned cDNA library prepared from heart of hibernating and summer animals"

ORIGIN

Query Match 91.2%; Score 366.8; DB 7; Length 779;
Best Local Similarity 94.5%; Pred. No. 2.3e-91;
Matches 380; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 ATGTGCAATACCAACATGTCTGTACTGATGAGTCTGTACACCTCAGATTC 60
125 ATGTGCAATACCAACATGTCTGTACTGATGAGTCTGTACACCTCAGATTC 184
61 GCTTCGGAACAGAGACCTGTGAGCCAAAGCCATGCTTTGAAGTATTAATCT 120
185 GCTTCGGAACAGAGACCTGTGAGCCAAAGCCATGCTTTGAAGTATTAATCT 244
121 GTTGTGACAAAAGACCTTATCTATGAGAGAGTCTTTTATCTTGGCCAGTAT 180
245 GTTGTGACAAAAGACCTTATCTATGAGAGAGTATTTTATCTTGGCCAGTAT 304
181 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGATTTGTCATATG 240
305 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGATTTGTCATATG 364
241 CTTCTGAGAGATTTGTTGGCGGCCAAGCTTCTCTGTAAGAGCAGAGAAATAT 300
365 CTTCTGAGAGATTTGTTGGAGTGCAGAGCTTCTCTGTAAGAGCAGAGAAATAT 424
301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGCAAGATCAGATCAGTACA 360
425 ACATGATCTACAGAAATTTGGTGTAGTCAATCAGAGCAACATCAGATTCAGACA 484
361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 402
485 TTAGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 526

RESULT 6
COT37954 858 bp mRNA linear EST 29-JUN-2004
LOCUS SLH03c19b19f1 squirrel heart library 1 *Spermophilus lateralis* cDNA
DEFINITION clone 19b19 5', mRNA sequence.
ACCESSION COT37954
VERSION COT37954.1 GI:50825224
KEYWORDS EST.
SOURCE *Spermophilus lateralis* (golden-mantled ground squirrel)

ORGANISM

Spermophilus lateralis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae; *Spermophilus*.

REFERENCE

1 (bases 1 to 858)
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W., Rogers, J., and Cossins, A.R.

TITLE Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, *Spermophilus lateralis*
JOURNAL Unpublished (2004)
COMMENT Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 19 row: b column: 19
Seq primer: pf1c t7 (5'-AATACGACTCACTATAGG-3')
High quality sequence stop: 858.
Location/Qualifiers

FEATURES

source

1..858
/organism="Spermophilus lateralis"
/mol_type="mRNA"
/db_xref="taxon:76772"
/clone="19b19"
/sex="Male & female"
/tissue_type="Heart"
/dev_stage="Adult"
/lab_host="E.coli Electromax DH10B"
/clone_1b="squirrel heart library 1"
/note="Vector: pFLC; Site 1: Sail GTCGAG; Site 2: BamHI GCATCC; Normalized and subcloned cDNA library prepared from heart of hibernating and summer animals"

ORIGIN

Query Match 91.2%; Score 366.8; DB 7; Length 858;
Best Local Similarity 94.5%; Pred. No. 2.4e-91;
Matches 380; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 ATGTGCAATACCAACATGTCTGTACTGATGAGTCTGTACACCTCAGATTC 60
160 ATGTGCAATACCAACATGTCTGTACTGATGAGTCTGTACACCTCAGATTC 219
61 GCTTCGGAACAGAGACCTGTGAGCCAAAGCCATGCTTTGAAGTATTAATCT 120
220 GCTTCGGAACAGAGACCTGTGAGCCAAAGCCATGCTTTGAAGTATTAATCT 279
121 GTTGTGACAAAAGACCTTATCTATGAGAGAGTCTTTTATCTTGGCCAGTAT 180
280 GTTGTGACAAAAGACCTTATCTATGAGAGAGTATTTTATCTTGGCCAGTAT 339
241 CTTCTGAGAGATTTGTTGGCGGCCAAGCTTCTCTGTAAGAGCAGAGAAATAT 300
340 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGATTTGTCATATG 399
181 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGATTTGTCATATG 240
340 ATTATGACTAAGCATTTATATGATGAGAGCAACATATTTGATTTGTCATATG 399
241 CTTCTGAGAGATTTGTTGGCGGCCAAGCTTCTCTGTAAGAGCAGAGAAATAT 300
400 CTTCTGAGAGATTTGTTGGAGTGCAGAGCTTCTCTGTAAGAGCAGAGAAATAT 459
301 ACCATGATCTACAGAACTTGTAGTATGATCAGAGCAAGATCAGATCAGTACA 360
460 ACATGATCTACAGAAATTTGGTGTAGTCAATCAGAGCAACATCAGATTCAGACA 519
361 TCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 402
520 TTAGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTAT 561

RESULT 7
BE900427

LOCUS BE900427 778 bp mRNA linear EST 29-SEP-2000
DEFINITION 601673652P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956413 5',
mRNA sequence.
ACCESSION BE900427
VERSION BE900427.1 GI:10388579
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 778)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov
Plate: LICM832 row: h column: 14
High quality sequence stop: 708.
Location/Qualifiers
1..778
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3956413"
/issue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source

Query Match 87.8%; Score 353; DB 2; Length 778;
Best Local Similarity 96.8%; Pred. No. 1.7e-87;
Matches 392; Conservative 0; Mismatches 10; Indels 3; Gaps 3;
ORIGIN
1 ATGTGCAATACCAATGCTGTACCTGATGAGTGTGCTGACCACTCAGATTCCA 60
288 ATGTGCAATACCAATGCTGTACCTGATGAGTGTGCTGACCACTCAGATTCCA 347
QY 61 GCTTCGGAACAAGAGACCTGCTTGAACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
348 GCTTCGGAACAAGAGACCTGCTTGAACCAAGCCATTGCTTTGAAGTTAAAGTCT 407
DB 121 GTTGTGACAAAAGACCTTATCTATGAAAGGCTTTTATCTTGGCCAGAT 180
408 GTTGTGACAAAAGACCTTATCTATGAAAGGCTTTTATCTTGGCCAGAT 467
QY 181 ATTAGCAATAAGCAATATATGATGAGAAACAACATATTTGATATGTTCAATGAT 240
468 ATTAGCAATAAGCAATATATGATGAGAAACAACATATTTGATATGTTCAATGAT 527
DB 241 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 299
528 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 587
QY 300 TACATAG-ATCTAGAGAACTTGAGTAGTC-AATGCGAGGAATCATCGGACTCGAGT 357
588 TACATAGATCTAGAGAACTTGAGTAGTC-AATGCGAGGAATCATCGGACTCGAGT 647
QY 358 ACATCTGATGAGAAAGAGGTGTCACTTGAAGGTGGAGTGAAT 402
|||||

DB 648 ACATCTGATGAGAAAGAGGTGTCACTTGAAGGTGGAGTGAAT 692

RESULT 8
LOCUS CO738288
DEFINITION CO738288 728 bp mRNA linear EST 29-JUL-2004
SILE04c20a14f1 squirrel embryo library 1 Spermophilus lateralis
cDNA clone 20a14 5', mRNA sequence.
ACCESSION CO738288
VERSION CO738288.1 GI:50825558
KEYWORDS EST.
SOURCE Spermophilus lateralis (golden-mantled ground squirrel)
ORGANISM Spermophilus lateralis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
Spermophilus.

REFERENCE 1 (bases 1 to 728)
AUTHORS Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W.,
Rogers, J. and Cossins, A.R.
TITLE Microarray analysis of transcriptional changes during hibernation
in the golden mantled ground squirrel, Spermophilus lateralis
Unpublished (2004)
JOURNAL Contact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@liv.ac.uk
Vector has been trimmed from this EST.
Plate: 20 row: a column: 14
Seq primer: p1c 77 (5'-AATGACCTCACTAATAGG-3')
High quality sequence stop: 728.
Location/Qualifiers

FEATURES
source

1..728
/organism="Spermophilus lateralis"
/mol_type="mRNA"
/db_xref="taxon:76772"
/clone="20a14"
/sex="male and female"
/issue_type="embryo"
/dev_stage="embryonic"
/lab_host="E.coli Electromax DH10B"
/clone_lib="squirrel embryo library 1"
/note="Vector: p1c; Site 1: SalI GTGAG; Site 2: BamHI
GATCC; Normalized and subcloned cDNA library prepared
from embryos"
ORIGIN
Query Match 86.5%; Score 347.6; DB 7; Length 728;
Best Local Similarity 93.8%; Pred. No. 5.3e-86;
Matches 362; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
1 ATGTGCAATACCAATGCTGTACCTGATGAGTGTGCTGACCACTCAGATTCCA 60
343 ATGTGCAATACCAATGCTGTACCTGATGAGTGTGCTGACCACTCAGATTCCA 402
QY 61 GCTTCGGAACAAGAGACCTGCTTGAACCAAGCCATTGCTTTGAAGTTAAAGTCT 120
403 GCTTCGGAACAAGAGACCTGCTTGAACCAAGCCATTGCTTTGAAGTTAAAGTCT 462
DB 403 GCTTCGGAACAAGAGACCTGCTTGAACCAAGCCATTGCTTTGAAGTTAAAGTCT 462
QY 121 GTTGTGACAAAAGACCTTATCTATGAAAGGCTTTTATCTTGGCCAGAT 180
463 GTTGTGACAAAAGACCTTATCTATGAAAGGCTTTTATCTTGGCCAGAT 522
DB 241 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 240
523 ATTAGCAATAAGCAATATATGATGAGAAACAACATATTTGATATGTTCAATGAT 582
QY 181 ATTAGCAATAAGCAATATATGATGAGAAACAACATATTTGATATGTTCAATGAT 240
523 ATTAGCAATAAGCAATATATGATGAGAAACAACATATTTGATATGTTCAATGAT 582
DB 241 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 300
583 CTCTAGAGATTGTTGGCGTGCAGAGCTTCTCTGTGA-AAGAGCAGAGAAATATA 642
|||||

QY 301 ACCATGATCTACAGAACTTGTAGTCAATGACAGAGAAATCGACTCAGATCA 360
DB 643 ACATGATCTACAAAAATTTGGTGTAGTCAATGACAGAGAAACATCAGATTCAGACCA 702
QY 361 TCTGTAGTGAAGAACAGGTGTACCT 386
DB 703 TTAGTGAAGTGAAGAACAGGTGTACCT 728

RESULT 9
LOCUS BE765314 345 bp mRNA linear EST 19-SEP-2000
DEFINITION IL2-NT0102-280700-115-H11 NT0102 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE765314
VERSION BE765314.1 GI:10195238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 345)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W.J.F., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Mateukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongseneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL2-NT0102-280
700-115-H11&t3=2000-07-28&t4=1)
Seg primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 344.
Location/Qualifiers
1..345
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_id="NT0102"
/note="Organ: nervous tumor; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 80.7%; Score 324.4; DB 2; Length 345;
Best Local Similarity 98.2%; Pred. No. 1.4e-79;
Matches 328; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGTGAATACCAACATGCTGTACTGATGATGCTGTAAACCACTCAGATTCGA 60
DB 12 AGGTGCAATACCAACATGCTGTACTGATGATGCTGTAAACCACTCAGATTCGA 71
QY 61 GCTTGGAAACAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAGTTAATTAAGTCT 120

DB 72 GCTTGGAAACAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAGTTAATTAAGTCT 131
QY 121 GTTGGACCAAAAAGACCTTATACATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
DB 132 GGTGATGCACAAAAGACCTTATACATGTAAGAGGTTCTTTTATCTTGCCAGTAT 191
QY 181 ATTATGACTAAAGATTATATGATGAGAAACAACATATTTATATTTGTAATGAT 240
DB 192 ATTATGACTAAAGATTATATGATGAGAAACAACATATTTATTTCTTCAATGAT 251
QY 241 CTTCTAGAGATTGTTGTTGGCGTGCAGAGCTTCTGTGTAAGAGACACAGAAATATAT 300
DB 252 CTTCTAGAGATTGTTGTTGGCGTGCAGAGCTTCTGTGTAAGAGACAGAAATATAT 311
QY 301 ACCATGATCTACAGAACTTGTAGTCAATGACAGAGAAATCGACTCAGATCA 334
DB 312 ACCATGATCTACAGAACTTGTAGTCAATGACAGAGAAATCGACTCAGATCA 345

RESULT 10
LOCUS AL704062 393 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686N1428 t1 686 (synonym: h1cc3) Homo sapiens CDNA clone
ACCESSION AL704062
VERSION AL704062.1 GI:19687417
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 393)
AUTHORS Otenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weill, B. and
Wiemann, S.
TITLE EST (Otenwaelder, B., Obermaier, B., Mewes, H.W., Weill, B. and
Wiemann, S.)
JOURNAL Unpublished (2001)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Cancer Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the CDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKFZp686N1428) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..393
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686N1428"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="686 (synonym: h1cc3)"
/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI;
cDNA-collection"

ORIGIN
Query Match 80.6%; Score 324; DB 1; Length 393;
Best Local Similarity 99.4%; Pred. No. 1.8e-79;
Matches 324; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGAATACCAACATGCTGTACTGATGATGCTGTAAACCACTCAGATTCGA 60
DB 68 ATGTGAATACCAACATGCTGTACTGATGATGCTGTAAACCACTCAGATTCGA 127
QY 61 GCTTGGAAACAGAGACCTGTGTTAGACCAAGCCATTGCTTTGAAGTTAATTAAGTCT 120

Db 128 GCTTCGAGACAGAGACCCTGTTAGACCAAGCCATTGCTTTGAATTATTAAGTCT 187
Qy 121 GTTGTGACACAAAGACCTTATATATGAAGGCTTTTATATCTGGCAGAT 180
Db 188 GNNGTGCACAAAAGACCTTATATATGAAGGCTTTTATATCTGGCAGAT 247
Qy 181 ATTATGACTAAACGATTATATATGATAGAGCAACACATATTGATATGTTCAATGAT 240
Db 248 ATTATGACTAAACGATTATATATGATAGAGCAACACATATTGATATGTTCAATGAT 307
Qy 241 CTCTAGAGATTGTTGGCGCCAGACTTCTCTGTGAAAGACACAGAAATATAT 300
Db 308 CTCTAGAGATTGTTGGCGCCAGACTTCTCTGTGAAAGACACAGAAATATAT 367
Qy 301 ACCATGATCTACAGGAAGCTGTAGT 326
Db 368 ACCATGATCTACAGGAAGCTGTAGT 393

RESULT 11
AI902188/c 518 bp mRNA linear EST 30-MAR-2000
LOCUS AI902188 11-BT002-221198-015 BT002 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI902188
VERSION AI902188.1 GI:6492666
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 518)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Mateukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800

TITLE Contact: Simpson A.J.G.
JOURNAL Laboratory of Cancer Genetics
MEDLINE Ludwig Institute for Cancer Research
PUBMED Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
COMMENT Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?i=11&t=11-BT002-015.html
&t3=221198&t4=1)
Seq primer: puc 18 forward.
FEATURES
source Location/Qualifiers
1..518
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_id="BT002"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 79.1%; Score 318; DB 1; Length 518;

Best Local Similarity 89.9%; Pred. No. 9e-78;
Matches 358; Conservative 0; Mismatches 38; Indels 2; Gaps 2;
Qy 5 GCATTAACCAAGCTCTGTAACCTAGATGCTGTAAACCACTCAGATTCAGCTT 64
Db 480 GCCATCCCAAAAGGTGNCNCTACTGANGGCTGGAACCACTTCAGATTCAGCTT 421
Qy 65 CGGAACAAGAGACCCCTGTTAGACCAAGCATGCTTTGAAGTTATTAAGCTGTTG 124
Db 420 GGAACCAAGAGCCCTGTTAGACCAAGCATGCTTTGAAGTTATTAAGCTGTTG 362
Qy 125 GTGCACAAAAGACACTTATATATGAGAGAGGTTCTTTTATCTTGGCAGATATTA 184
Db 361 GTGCNC-AAAAGNCATATATATGAGAGAGGCTTTTATATCTTGGCAGATATTA 303
Qy 185 TGACTAAAGATTTATATGATGAGAGCAACATATTTATATGTTCAATGATCTTC 244
Db 302 TGACTAAAGATTTATATGATGAGAGCAACATATTTATATGTTCAATGATCTTC 243
Qy 245 TAGAGATTGTTGGCGCCAGACTTCTCTGTGAAAGACACAGAAATATATATCA 304
Db 242 TAGAGATTGTTGGCGCCAGACTTCTCTGTGAAAGACACAGAAATATATATCA 183
Qy 305 TGAATCTACAGAACTTGTAGTATGATCAATGAGAGCAATCATCGACTCAGTATCTG 364
Db 182 TGAATCTACAGAACTTGTAGTATGATCAATGAGAGCAATCATCGACTCAGTATCTG 123
Qy 365 TGAATCTACAGAACTTGTAGTATGATCAATGAGAGCAATCATCGACTCAGTATCTG 402
Db 122 TGAATCTACAGAACTTGTAGTATGATCAATGAGAGCAATCATCGACTCAGTATCTG 85

RESULT 12
CN409877 400 bp mRNA linear EST 16-MAY-2004
LOCUS CN409877 17000418214393 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN409877
ACCESSION CN409877
VERSION CN409877.1 GI:47397001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 400)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 400 Std Error: 0.00.
FEATURES
source Location/Qualifiers
1..400
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_id="GRN EB"
/note="Toigo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 77.1%; Score 310; DB 7; Length 400;

Best Local Similarity 99.7%; Pred. No. 1.5e-75;
Matches 321; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 81 GGTAGACCAAGCATTTGTTTGAAGTATTAAGTCGTGGTCACAAAAGAC 140
DB 2 GGTAGACCAAGCATTTGTTTGAAGTATTAAGTCGTGGTCACAAAAGAC 60
QY 141 TTATATATGAAAGAGTTCTTTTATCTTGGCAGTATATTAAGCATTTA 200
DB 61 TTATATATGAAAGAGTTCTTTTATCTTGGCAGTATATTAAGCATTTA 120
QY 201 TGTATGACCAACACATATTTGTATTTGTTCAATGATCTTACAGATTTGTTGG 260
DB 121 TGTATGACCAACACATATTTGTATTTGTTCAATGATCTTACAGATTTGTTGG 180
QY 261 CGGCCAAGCTTCTCTGTGAAGAGCAGAGAAATATATACATGATCTACAGAACTT 320
DB 181 CGGCCAAGCTTCTCTGTGAAGAGCAGAGAAATATATACATGATCTACAGAACTT 240
QY 321 GGTAGTATGATCATCAGACGAATCATCGACTCAGTACATCTGTGAGTGAACAGGTG 380
DB 241 GGTAGTATGATCATCAGACGAATCATCGACTCAGTACATCTGTGAGTGAACAGGTG 300
QY 381 TCACCTTGAAGGTGGAGTAT 402
DB 301 TCACCTTGAAGGTGGAGTAT 322

RESULT 13
BF683210 1008 bp mRNA linear EST 22-DEC-2000
LOCUS 602139233F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298285 5',
DEFINITION mRNA sequence.

ACCESSION BF683210 GI:11968618
VERSION BF683210
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1008)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCMI53 row: m column: 06
High quality sequence stop: 697.
Location/Qualifiers

FEATURES
source 1..1008
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4298285"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.0%; Score 297.4; DB 2; Length 1008;
Best Local Similarity 81.0%; Pred. No. 5.8e-72;
Matches 401; Conservative 0; Mismatches 1; Indels 93; Gaps 1;

QY 1 ATGTGCAATTCACCAATGCTCTGTAAGTATGATGCTGTTAAACCACTCAGATTTCCA 60
DB 56 ATGTGCAATTCACCAATGCTCTGTAAGTATGATGCTGTTAAACCACTCAGATTTCCA 115
QY 61 GCTTGGCAACAGAGCCCTGGTTAGACCAAGCCCTGTTGAAGTATTAAGTCT 120
DB 116 GCTTGGCAACAGAGCCCTGGTTAGACCAAGCCCTGTTGAAGTATTAAGTCT 175
QY 121 GTTGTGCACAAAAAGACATTATATGAAG----- 154
DB 176 GTTGTGCACAAAAAGACATTATATGAAGAAGATGAGTTCACTATGTTGCC 235
QY 155 ----- 154
DB 236 AGGCTGATCTGAACTCTGGGCTCAAGGATCTGCTACCTGGCCTCTAAAGTCTA 295
QY 155 -----AGTTCTTTTATATCTTGGCCAGTATATTAAGTAAAGATTAATGATGAG 207
DB 296 GATTACAGGTTCTTTTATATCTTGGCCAGTATATTAAGTAAAGATTAATGATGAG 355
QY 208 AAGCAACAACATATTTGATATTTGTTCAATGATCTTCTAGAGATTTGTTGGCGTCCA 267
DB 356 AAGCAACAACATATTTGATATTTGTTCAATGATCTTCTAGAGATTTGTTGGCGTCCA 415
QY 268 AGCTTCTCTGTGAAGAGCAGAGAAATATATATCATGATCTTCTACAGAACTTGTAGTA 327
DB 416 AGCTTCTCTGTGAAGAGCAGAGAAATATATATCATGATCTTCTACAGAACTTGTAGTA 475
QY 328 GTCATACAGAGAAATCATCGACTCAGTACATCTGTGAGTGAACAGGTGTCACCTT 387
DB 476 GTCATACAGAGAAATCATCGACTCAGTACATCTGTGAGTGAACAGGTGTCACCTT 535
QY 388 GAAGGTGGAGTAT 402
DB 536 GAAGGTGGAGTAT 550

RESULT 14
BF114786 507 bp mRNA linear EST 24-OCT-2000
LOCUS BF114786
DEFINITION 7367806.X1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3391499 3' similar to SW:MDM2_HUMAN Q00987 MDM2 PROTEIN ;,
mRNA sequence.

ACCESSION BF114786 GI:10984262
VERSION BF114786
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 507)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 474.
Location/Qualifiers

FEATURES
source 1..507
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3391499"

/lab_host="DH10B"
/clone_1lb="Soares NSF P8 9W OT PA P S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHP pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HP-9W pool 1:
758280-760583, 772104-774407 Soares NBHP pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHP
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 507;
Best Local Similarity 95.6%; Pred. No. 3.1e-71;
Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTTACTGATGCTGTAAACACCTCAGATTCCA 60
DB 185 ATGTGCAATACCAACATGTCTGTACTTACTGATGCTGTAAACACCTCAGATTCCA 244
QY 61 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 245 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 304
QY 121 GTTGTGACAAAAAGACACTTATCATAGAAAGGTTCTTTTATCTTGGCAGATAT 180
DB 305 GTTGTGACAAAAAGACACTTATCATAGAAAGGTTCTTTTATCTTGGCAGATAT 364
QY 181 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGATATTTGTTCAATGAT 240
DB 365 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGATATTTGTTCAATGAT 424
QY 241 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGACACAGAAAAATATAT 300
DB 425 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGACACAGAAAAATATAT 484
QY 301 ACCATGATCTACAGGAA 317
DB 485 AGTTAGTCCATTGTAA 501

RESULT 15

BP435134 512 bp mRNA linear EST 19-JAN-2001
LOCUS nab43b10.x1 Soares NSF P8 9W OT PA P S1 Homo sapiens cDNA clone
DEFINITION IMAGE:3268553 similar to SW:MDM2_HUMAN Q00987 MDM2 PROTEIN ;
mRNA sequence.

ACCESSION BP435134
VERSION BP435134.1 GI:11447422
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 452.

FEATURES
source

Location/Qualifiers
1..512
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3268553"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHP pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HP-9W pool 1:
758280-760583, 772104-774407 Soares NBHP pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHP
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 512;
Best Local Similarity 95.6%; Pred. No. 3.1e-71;
Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGTGCAATACCAACATGTCTGTACTTACTGATGCTGTAAACACCTCAGATTCCA 60
DB 186 ATGTGCAATACCAACATGTCTGTACTTACTGATGCTGTAAACACCTCAGATTCCA 245
QY 61 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 120
DB 246 GCTTGGACACAGAGACCTGTGTAGACCAAGCCATTGCTTTGAAGTTATTAAGTCT 305
QY 121 GTTGTGACAAAAAGACACTTATCATAGAAAGGTTCTTTTATCTTGGCAGATAT 180
DB 306 GTTGTGACAAAAAGACACTTATCATAGAAAGGTTCTTTTATCTTGGCAGATAT 365
QY 181 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGATATTTGTTCAATGAT 240
DB 366 ATTATGACTAAACGATTATATGATGAGAACCAACATATTTGATATTTGTTCAATGAT 425
QY 241 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGACACAGAAAAATATAT 300
DB 426 CTTCTAGAGATTGTTGGCGTCCAGAGCTTCTCTGTGAAGACACAGAAAAATATAT 485
QY 301 ACCATGATCTACAGGAA 317
DB 486 AGTTAGTCCATTGTAA 502

Search completed: October 18, 2004, 14:51:57
Job time : 7339 secs

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